

OM of: US-09-198-779b-1 to: A\_Geneseq\_032802:\* out\_format : pfs  
 Date: Aug 20, 2002 2:57 AM  
 About: Results were produced by the Gencore software, version 4.5,  
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Command line parameters:  
 -MODEL=frame+np.model -DEV=xlip  
 -O=/gen2.1/USPRO.spool/US09198779/runat\_19082002.140911.25072/app-query.fasta.1.296  
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 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct  
 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pfs  
 -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
 -USER=US09198779 -SCGNL\_1\_72 -NCPU=6 -ICPU=3 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLIPXY -WAIT -THREADS=1

Search information block:  
 Query: US-09-198-779b-1  
 Query length: 235  
 Database: A\_Geneseq\_032802:\*  
 Database sequences: 747574  
 Database length: 11073796  
 Search time (sec): 54.720000

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KW hybridisation assay; genetic mapping; gene expression control; promoter;			
KW termination sequence; corn.			
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OS Zea mays subsp. mays.			
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PD 06-SEP-2000.			
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US-09-198-779b-1 x AAG43923 ..

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DT 18-OCT-2000 (first entry)  
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KW Protein identification; signal transduction pathway; metabolic pathway;  
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PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.

PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155186.  
PR 24-SEP-1999; 99US-0155486.  
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PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
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PR 22-OCT-1999; 99US-0160980.  
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PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 25-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

## alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

## alignment\_block:

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311 ATGPhelIeIySThrIaIaIaTyTgIyHISPhelIyAqAsPaSPaIaAs 327  
210 CTTACCTGCGAGGTGTCACGCC 234  
|||||  
327 pPhetHrTPgIuValIyIySPe 335  
seq\_name: /SIDSL/gcgdata/geneseq/geneseq\_emb1/AAG2000.DAT.AAG43921  
seq\_documentation\_block:  
ID AAG43921 standard; Protein: 392 AA.  
XX  
AC AAG43921;  
DT 18-OCT-2000 (first entry)  
XX  
DE Zea mays protein fragment SEQ ID NO: 54955.  
XX  
KW Protein identification: signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence; corn.  
XX  
OS Zea mays subsp. mays.  
XX  
PM EP1033405-A2.  
XX  
ED 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
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PR 23-APR-1999; 99US-0130891.  
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PR 30-APR-1999; 99US-0132407.  
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PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
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PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.



PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
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PR 06-JUL-1999; 99US-0142390.  
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PR 19-JUL-1999; 99US-0144331.  
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PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
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PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
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PR 20-AUG-1999; 99US-0149723.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151338.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
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PR 20-SEP-1999; 99US-0154779.  
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PR 28-SEP-1999; 99US-0156458.  
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PR 07-OCT-1999; 99US-0158029.  
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PR 14-OCT-1999; 99US-0159637.  
PR 18-OCT-1999; 99US-0159638.  
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PR 21-OCT-1999; 99US-0160741.  
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PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
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PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

alignment\_scores:

Quality: 127.00

Ratio: 5.292

Length:

Gaps:

25  
0

Percent Similarity: 96.000 Percent Identity: 96.000

# alignment\_block:

US-09-198-779B-1 x AAW343921 ..

Align seg 1/1 to: AAW343921 from: 1 to: 392

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362 ArgPheIleLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspAlaAs 378
210 CTTGACCTGCGAGGTGGTCAAGCCC 234
    |||||||
378 pPheHtrTrpGluValValLysPro 386

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seq\_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:AAW34540

# seq\_documentation\_block:

ID AAW34540 standard; protein: 394 AA.

AC AAW34540;

XX 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 1.

XX S-adenosylmethionine synthase 1; sam1; barley; alkali resistant plant.

OS Hordeum vulgare.

XX JP09313186-A.

XX 09-DEC-1997.

XX 28-MAY-1996; 96JP-0133406.

XX 28-MAY-1996; 96JP-0133406.

XX (NIOC ) NIPPON OIL CO LTD.

XX WPI: 1998-080077/08.

DR N-PSDB: AAT99141.

PT S-adenosyl-methionine synthase gene - useful in producing plants resistant to alkaline soil

XX Claim 1; Page 5-6; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 1 (sam1) protein. The DNA encoding this sequence may be used in producing plants which are resistant to alkaline soil.

XX Sequence 394 AA;

# alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

# alignment\_block:

US-09-198-779B-1 x AAW34540 ..

Align seg 1/1 to: AAW34540 from: 1 to: 394

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160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
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362 ArgPheIleLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspAlaAs 378
210 CTTGACCTGCGAGGTGGTCAAGCCC 234
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378 pPheHtrTrpGluValValLysPro 386

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seq\_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:AAW34541

# seq\_documentation\_block:

ID AAW34541 standard; protein: 394 AA.

AC AAW34541;

XX 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 2.

XX S-adenosylmethionine synthase 2; sam2; barley; alkali resistant plant.

OS Hordeum vulgare.

XX JP09313186-A.

XX 09-DEC-1997.

XX 28-MAY-1996; 96JP-0133406.

XX 28-MAY-1996; 96JP-0133406.

XX (NIOC ) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.

DR N-PSDB: AAT99142.

PT S-adenosyl-methionine synthase gene - useful in producing plants resistant to alkaline soil

XX Claim 2; Page 6-7; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 2 (sam2) protein. The DNA encoding this sequence may be used in producing plants which are resistant to alkaline soil.

XX Sequence 394 AA;

# alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

# alignment\_block:

US-09-198-779B-1 x AAW34541 ..

Align seg 1/1 to: AAW34541 from: 1 to: 394

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160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
    |||||||
362 ArgPheIleLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspAlaAs 378
210 CTTGACCTGCGAGGTGGTCAAGCCC 234
    |||||||
378 pPheHtrTrpGluValValLysPro 386

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seq\_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:AAW34542

# seq\_documentation\_block:

ID AAW34542 standard; protein: 394 AA.

AC AAW34542;

XX 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 3.

XX S-adenosylmethionine synthase 3; sam3; barley; alkali resistant plant.

OS Hordeum vulgare.

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PN JP09313186-A.
XX
PD 09-DEC-1997.
XX
PF 28-MAY-1996; 96JP-0133406.
XX
PR 28-MAY-1996; 96JP-0133406.
XX
PA (NIOC ) NIPPON OIL CO LTD.
XX
DR WPI; 1998-080077/08.
XX
DR N-PSDB; AAT99143.
XX
PT S-adenosyl-methionine synthase gene - useful in producing plants
XX resistant to alkaline soil
PS Claim 3; Page 7-8; 13pp; Japanese.
XX
CC This sequence represents the S-adenosylmethionine synthase 3 (sam3)
CC protein. The DNA encoding this sequence may be used in producing plants
CC which are resistant to alkaline soil.
XX
SQ Sequence 394 AA:

alignment_scores:
  Quality: 127.00 Length: 25
  Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x AAW34542 ..

Align seg 1/1 to: AAW34542 from: 1 to: 394

160 AGGTTTCATCAAGACCGCGCATACGGCCATTGGCCGTGACGACCGCA 209
|||||
362 ArgpheiIeLysThrAlaAlaIatyrGlyHisPheGlyArgAspAlaAs 378
210 CTTCACTGCGAGGTGTCAGCC 234
|||||
378 pPheThrTrpGluValValLysPro 386

seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:AAW97744

seq_documentation_block:
ID AAW97744 standard; Protein; 394 AA.
XX
AC AAW97744;
XX
DT 21-MAY-1999 (first entry)
XX
DE wheat S-adenosylmethionine synthetase.
XX
KW S-adenosylmethionine synthetase; wheat; amino acid; lysine;
KW threonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff.
XX
OS Triticum aestivum.
XX
FH Key Location/Qualifiers
FT Misc-difference 93 /note- "encoded by AAR"
FT Misc-difference 150 /note- "encoded by CTY"
FT Misc-difference 155 /note- "encoded by ACS"
FT Misc-difference 282 /note- "encoded by CGY"
FT Misc-difference 290 /note- "encoded by CAR"
XX
PN W09855601-A2.

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PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98MO-US11692.
XX
PR 12-JUN-1997; 97OS-0049443.
XX
PR 06-JUN-1997; 97US-0048771.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Abell LM, Allen SM, Falco SC, Hiltz WD, Kinney AJ;
PI Rafalski JA, Thorpe CJ;
XX
DR WPI; 1999-070263/06.
XX
DR N-PSDB; AAX07185.
XX
PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT encode: dihydrodipicolinate reductase; diaminopimelate epimerase;
PT threonine synthase; threonine deaminase; S-adenosylmethionine
PT synthetase
XX
PS Example 7; Page 70-71; 98pp; English.
XX
CC This is the amino acid sequence of a full-length wheat
CC S-adenosylmethionine synthetase, as deduced from a cDNA contig (see
CC AAX07185) obtained from kernel, leaf, seedling and root cDNA clones.
CC The wheat enzyme shows sequence similarity to the barley enzyme.
CC The invention relates to new isolated nucleic acid fragments (see
CC AAX07168-85) encoding plant enzymes (see AAW97727-44) that catalyze
CC steps in the biosynthesis of lysine, threonine, methionine,
CC cysteine and isoleucine from aspartate, the enzyme being selected
CC from dihydrodipicolinate reductase, diaminopimelate epimerase,
CC threonine synthase, threonine deaminase or S-adenosylmethionine
CC synthetase. The invention also relates to the construction of a
CC chimeric gene encoding all or a portion of the biosynthetic pathway
CC enzyme, in sense or antisense orientation, where expression of the
CC chimeric gene results in production of altered levels of the enzyme
CC in a transformed host cell. Overexpression or reduction of
CC expression of genes encoding the amino acid biosynthetic pathway
CC enzymes in crop plants such as corn, soybean and wheat can be used
CC to alter levels of the amino acids in human food and animal feed.
CC Transformed host cells can also be used to identify compounds that
CC inhibit one of the enzymes.
XX
SQ Sequence 394 AA:

alignment_scores:
  Quality: 127.00 Length: 25
  Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x AAW97744 ..

Align seg 1/1 to: AAW97744 from: 1 to: 394

160 AGGTTTCATCAAGACCGCGCATACGGCCATTGGCCGTGACGACCGCA 209
|||||
362 ArgpheiIeLysThrAlaAlaIatyrGlyHisPheGlyArgAspAlaAs 378
210 CTTCACTGCGAGGTGTCAGCC 234
|||||
378 pPheThrTrpGluValValLysPro 386

seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AA634556

seq_documentation_block:
ID AAG34556 standard; Protein; 47 AA.
XX
AC AAG34556;
XX
DT 18-OCT-2000 (first entry)
XX

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XX	Arabidopsis thaliana protein fragment SEQ ID NO: 42065.	PR	21-JUN-1999;	99US-0139817.
DE		PR	22-JUN-1999;	99US-0139899.
XX	Protein identification: signal transduction pathway; metabolic pathway;	PR	23-JUN-1999;	99US-0140353.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	PR	23-JUN-1999;	99US-0140354.
KW	termination sequence.	PR	24-JUN-1999;	99US-0140695.
XX		PR	28-JUN-1999;	99US-0140823.
XX	Arabidopsis thaliana.	PR	29-JUN-1999;	99US-0140991.
OS		PR	30-JUN-1999;	99US-0141287.
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XX		PR	01-JUL-1999;	99US-0142154.
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Ratio: 5.208 Caps: 0  
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310 ArgpHeLeUysThrAlaIaIaTyrgLyHsPneGlyAArgAspaSAlaAs 326  
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DE Arabidopsis thaliana protein fragment SPO ID NO: 5037.  
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XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
OS Arabidopsis thaliana.  
PN EP1033405-A2.  
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Percent Similarity: 96.000           Percent Identity: 92.000

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18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 46640.

Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.  
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PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
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KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

OS Arabidopsis thaliana.

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ID AAY21978 standard; Protein; 64 AA.
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XX AAY21978;
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DT 06-SEP-1999 (first entry)
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```
DE S-adenosyl methionine (SAM) partial sequence.
```

```
XX Sensence-associated receptor-like protein kinase; sark; sam gene; sag;
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```
KW Sensence-associated gene; plant senescence; promoter; pharmaceutical;
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KW plant maturation; S-adenosyl methionine; flower; fruit development.
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XX Phaseolus vulgaris.
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XX WO9929159-A1.
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PD 17-JUN-1999.
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PF 08-DEC-1998; 98WO-US25799.
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XX 08-DEC-1997; 97US-0067898.
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```
PR (VITA-) VITALITY BIOTECHNOLOGIES INC.
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XX Gepstein S, Hajuoje T, Rosner A;
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PI WPI: 1999-404873/34.
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```
DR N-PSDB; AAX81128.
```

```
PT DNA encoding senescence-associated genes for a senescence
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```
PT receptor-like protein kinase
```

```
PS Example 1; Fig 4; 70pp; English.
```

The invention relates to a senescence-associated receptor-like protein kinase (sark) gene. The sark gene is a senescence-associated gene (sag) and is expressed early in the plant senescence process. The sark gene promoter is useful for driving expression of foreign genes having a desired product, such as a pharmaceutical, during the process of plant maturation. The sark gene promoter can be used to drive expression of resistance genes against pathogens or pests during senescence when the plant is particularly susceptible to infection or infestation. The sark gene promoter may also be used to drive expression of a gene encoding an inhibitor of senescence. Plant senescence may be inhibited by use of antisense sark constructs. Over expression of the sag genes, using the sark or sam (S-adenosyl methionine) gene promoters is useful for induction of early senescence. This is useful to obtain flower or fruit development prior to specific pest onset, prior to undesirable cross-fertilization from related crops, at a specific time during storage or retail, or to avoid development of plant structures that are not of agronomic importance. The present sequence represents a partial sequence of S-adenosyl methionine (SAM).

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Sequence 64 AA:
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XX 17-OCT-2000 (first entry)  
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XX Protein identification: signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
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PR 29-OCT-1999; 99US-0162142.

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Ratio:	5.217	Gaps:	0
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US-09-198-779b-1 x AAG06585

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312 ArgPheLeuIysThrAlaIaIaTyRGLYHISPhGlyARgspsProAs 328  
210 CTTGACCTCGAGGTGTCAAGCCC 234  
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XX AAG06584;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 3409.

KM Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

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XX PR 06-APR-1999; 99US-0128234.

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PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.



```
CC AAW97727-44) that catalyse steps in the biosynthesis of lysine,
CC theonine, methionine, cysteine and isoleucine from aspartate, the
CC enzyme being selected from dihydrodipicolinate reductase,
CC diaminopimelate epimerase, threonine synthase, threonine deaminase
CC or S-adenosylmethionine synthetase. The invention also relates to
CC the construction of a chimeric gene encoding all or a portion of
CC the biosynthetic pathway enzyme, in sense or antisense orientation,
CC where expression of the enzyme in a transformed host cell.
CC altered levels of the enzyme in a transformed host cell.
CC Overexpression or reduction of expression of genes encoding the
CC amino acid biosynthetic pathway enzymes in crop plants such as
CC corn, soybean and wheat can be used to alter levels of the amino
CC acids in human food and animal feed. Transformed host cells can
CC also be used to identify compounds that inhibit one of the enzymes.
XX
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DT 21-MAY-1999 (first entry)
XX
DE Soybean S-adenosylmethionine synthetase.
XX
KW S-Adenosylmethionine synthetase; soybean; amino acid; lysine;
KW theonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff.
XX
OS Glycine max.
XX
PN WO9855601-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11692.
XX
PR 12-JUN-1997; 97US-0049443.
PR 06-JUN-1997; 97US-0048771.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Abell LM, Allen SM, Falco SC, Hiltz WD, Kinney AJ;
PI Rafalski JA, Thorpe CJ;
XX
DR WPI: 1999-070263/06.
DR N-PSDB: AAX07184.
XX
PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT encode: dihydrodipicolinate reductase; diaminopimelate epimerase;
PT theonine synthase; threonine deaminase; S-adenosylmethionine
```

```
PT synthetase
XX
XX Example 7; Page 67-68; 98pp; English.
XX
CC This is the amino acid sequence of a full-length soybean
CC S-adenosylmethionine synthetase, as deduced from a cDNA clone (see
CC AAX07184), designated s2.12b06, obtained from a soybean seed
CC cDNA library. The soybean enzyme shows sequence similarity to the
CC tomato enzyme. The invention relates to new isolated nucleic acid
CC fragments (see AAX07168-85) encoding plant enzymes (see AAW97727-44)
CC that catalyse steps in the biosynthesis of lysine, threonine,
CC methionine, cysteine and isoleucine from aspartate, the enzyme
CC being selected from dihydrodipicolinate reductase,
CC diaminopimelate epimerase, threonine synthase, threonine deaminase
CC or S-adenosylmethionine synthetase. The invention also relates to
CC the construction of a chimeric gene encoding all or a portion of
CC the biosynthetic pathway enzyme, in sense or antisense orientation,
CC where expression of the chimeric gene results in production of
CC altered levels of the enzyme in a transformed host cell.
CC Overexpression or reduction of expression of genes encoding the
CC amino acid biosynthetic pathway enzymes in crop plants such as
CC corn, soybean and wheat can be used to alter levels of the amino
CC acids in human food and animal feed. Transformed host cells can
CC also be used to identify compounds that inhibit one of the enzymes.
XX
SQ Sequence 392 AA;

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    Ratio: 5.043        Gaps: 0
    Percent Similarity: 92.000    Percent Identity: 84.000

alignment_block:
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210 CTTTCACCTGCGAGGTGGTCAAGCCC 234
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seq_documentation_block:
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AC AA606945;
XX
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3909.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
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PR 06-APR-1999; 99US-0128234.  
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PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
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PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
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PR 28-JUL-1999; 99US-0145951.  
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PR 27-AUG-1999; 99US-0151083.  
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PR 04-OCT-1999; 99US-0157117.  
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alignment\_block:  
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Align seg 1/1 to: AAG06945 from: 1 to: 311

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210 CTTCACTCGGAGTGTGTCAAGCCC 234  
||||| ||||||| ||||||| ||||||| ||||||| ||  
295 PheThrTrpGluValIaIaLysPro 303

seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.AAG39109

seq\_documentation\_block:

ID AAG39109 standard; Protein: 341 AA.

XX AAG39109;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 48343.

XX Protein identification: signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.  
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PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
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PR 30-APR-1999; 99US-0132048.  
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PR 03-AUG-1999; 99US-0147038.
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PR 29-OCT-1999; 99US-0162142.
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  Ratio: 5.227
  Percent Similarity: 88.000
  Percent Identity: 88.000
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AC AAG40368;
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XX
DT 18-OCT-2000 (first entry)
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XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50079.
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KW protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX
OS Arabidopsis thaliana.
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XX
PN EP1033405-A2.
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XX
PD 06-SEP-2000.
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XX   17-OCT-2000 (first entry)

XX   Arabidopsis thaliana protein fragment SEQ ID NO: 3908.

DE   Protein identification; signal transduction pathway; metabolic pathway;  
KW   hybridisation assay; genetic mapping; gene expression control; promoter;  
KW   termination sequence.

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ID AAG06943 standard; Protein: 368 AA.

XX AAG06943;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 3907.

XX Protein identification, signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS EP1033405-A2.  
XX 06-SEP-2000.  
PD 25-FEB-2000; 2000EP-0301439.  
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seq\_documentation\_block:  
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XX 18-OCT-2000 (first entry)  
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 48342.
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KW	hybridisation assay; genetic mapping; gene expression control; promoter,
KM	termination sequence.
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PR	17-AUG-1999	9905-0149175
PR	18-AUG-1999	9905-0149426
PR	20-AUG-1999	9905-0149722
PR	20-AUG-1999	9905-0149723
PR	20-AUG-1999	9905-0149929
PR	23-AUG-1999	9905-0149992
PR	23-AUG-1999	9905-0149930
PR	25-AUG-1999	9905-0150566
PR	26-AUG-1999	9905-0150684

PR	27-ANG-1999;	9905-0151065
PR	27-ANG-1999;	9905-0151066
PR	27-AUG-1999;	9905-0151080
PR	30-ANG-1999;	9905-0151303
PR	31-ANG-1999;	9905-0151308
PR	01-SEP-1999;	9905-0151930
PR	07-SEP-1999;	9905-0152363
PR	10-SEP-1999;	9905-0153070
PR	13-SEP-1999;	9905-0153758
PR	15-SEP-1999;	9905-0154040
PR	16-SEP-1999;	9905-0154039
PR	20-SEP-1999;	9905-0154779
PR	22-SEP-1999;	9905-0155139
PR	23-SEP-1999;	9905-0155486
PR	24-SEP-1999;	9905-0155569
PR	28-SEP-1999;	9905-0156458
PR	29-SEP-1999;	9905-0156596
PR	04-OCT-1999;	9905-0157177
PR	05-OCT-1999;	9905-0157753
PR	06-OCT-1999;	9905-0157865
PR	07-OCT-1999;	9905-0158032
PR	08-OCT-1999;	9905-0158239
PR	12-OCT-1999;	9905-0158363
PR	13-OCT-1999;	9905-0159293
PR	13-OCT-1999;	9905-0159294
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PR	14-OCT-1999;	9905-0159329
PR	14-OCT-1999;	9905-0159331
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PR	21-OCT-1999;	9905-0160815
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PR	25-OCT-1999;	9905-0161405
PR	25-OCT-1999;	9905-0161406
PR	26-OCT-1999;	9905-0161359
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PR	28-OCT-1999;	9905-0161920
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PR	29-OCT-1999;	9905-0162142

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Percent Similarity:      88.000 Percent Identity: 88.000
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alignment\_block:

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160 AGGTTATCAACAGACCGCCGCAATGCGCCACTTTGGCCCGCGACAGCCGA 209  
361 ArgPheGlnLysTrpAlaAlaLysLysPheGlyArgGlnPheProAsp 377			
210 CTTCAACCTGCGAGGTGTGTCAGGCC 234			
377 pPheThrTrpGlnValValLysPro 385			

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seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AA639107
seq_documentation_block:
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ID AAG39107 standard; Protein; 439 AA.  
XX AAG39107;  
AC  
XX  
DT 18-OCT-2000 (first entry)  
XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 48341.  
DE  
XX Protein identification: signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS  
XX EPI033405-A2.  
PN  
XX  
PD 06-SEP-2000.  
XX  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129645.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130049.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
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PR 06-MAY-1999; 99US-0132485.  
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PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 14-JUN-1999; 99US-0138847.  
PR 16-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 17-JUN-1999; 99US-0139453.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 24-JUN-1999; 99US-0140354.  
PR 28-JUN-1999; 99US-0140695.  
PR 29-JUN-1999; 99US-0140823.  
PR 30-JUN-1999; 99US-0140991.  
PR 01-JUL-1999; 99US-0141287.  
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PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143542.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
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PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
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PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
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PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
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PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 05-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147303.  
PR 09-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 10-AUG-1999; 99US-0147935.  
PR 11-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148341.  
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PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.

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PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 07-OCT-1999; 99US-0158029.
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PR 12-OCT-1999; 99US-0158363.
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PR 14-OCT-1999; 99US-0159295.
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PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160770.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161400.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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alignment_scores:
  Quality: 115.00      Length: 25
  Ratio: 5.227         Gaps: 0
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160 AGGTTTCATCAGACCGCGCATATGAGCCACTTTGGCCGTGACAGCCGA 209
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410 ArgpHeGlnLysThrAlaIatYrgLHsPheGlyArgAspAspProAs 426
210 CTTCACTCGGAGGAGGTGTCAAGCCC 234
||||| ||||||| ||||||| ||
426 pPheThrTrpGluValValLysPro 434

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seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAV72078
seq_documentation_block:
  ID AAV72078 standard: Protein; 390 AA.

```

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  AAV72078;

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  28-MAR-2001 (first entry)

```

```

  Nicotiana tabacum S-adenosylmethionine synthetase (SAMS).

```

```

  Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
  herbicide resistance; S-adenosylmethionine synthetase; SAMS.

```

```

  Nicotiana tabacum.

```

```

  WO200067558-A1.

```

```

  16-NOV-2000.

```

```

  05-MAY-2000; 2000WO-US12450.

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  06-MAY-1999; 99US-0132919.

```

```

  (TIMK/) TIMKO M.

```

```

  Timko M;

```

```

  WPI: 2001-007279/01.

```

```

  N-PSDB; AAD02296.

```

```

  New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
  e.g. for producing transgenic plants with altered nicotine content.

```

```

  Claim 17; Page 79-81; 103pp; English.

```

```

  The invention relates to enzymes involved in alkaloid, specifically
  nicotine, synthesis in tobacco and nucleic acids encoding them. The
  nucleic acid of the invention can be used, in sense or antisense
  orientation, to produce transgenic tobacco plants with altered
  alkaloid content, and also for expression of exogenous proteins,
  e.g. pharmaceutical proteins or proteins implicated in resistance
  to herbicides. The protein of the invention can be used to
  CC Identify modulators of enzymatic activity in plants.
  CC The present sequence is Nicotiana tabacum S-adenosylmethionine
  CC synthetase (SAMS). This enzyme is involved in the nicotine
  CC biosynthetic pathway.

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  Sequence 390 AA;

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alignment_scores:
  Quality: 97.00      Length: 24
  Ratio: 4.619         Gaps: 0
  Percent Similarity: 87.500  Percent Identity: 75.000

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alignment_block:
  us-09-198-779b-1 x AAV72078 ..

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Align seg 1/1 to: AAV72078 from: 1 to: 390

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361 ArgTYrGlnLysThrAlaIatYrgLHsPheGlyArgAspAspProAs 377
210 CTTCACTCGGAGGAGGTGTCAAG 231
||||| ||||||| ||||||| ||
377 pPheSerTrpGluThrValLys 384

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```

seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AAI18652
seq_documentation_block:
  ID AAI18652 standard: Protein; 332 AA.

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XX AC AAB18652:
XX XX
XX DT 22-JAN-2001 (first entry)
XX XX
DE Amino acid sequence of an ORF15 partial S-adenosylmethionine synthase.
XX XX
XX KM Nardoniolide synthase; polyketide synthase gene; nardoniolide polyketide;
XX KM antibiotic; C12-hydroxylase; pick; desosamine biosynthesis;
XX KM desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;
XX KM picromycin biosynthesis; S-adenosylmethionine synthase.
XX OS
XX OS Streptomyces venezuelae.
XX PN
XX PN US6117659-A.
XX PD
XX PD 12-SEP-2000.
XX XX
XX PF 27-MAY-1999; 99US-0320878.
XX XX
XX PR 28-MAY-1998; 98US-0087080.
XX PR 22-SEP-1998; 98US-0100880.
XX PR 08-FEB-1999; 99US-0119139.
XX PR 20-MAY-1999; 99US-0134990.
XX PR 30-APR-1997; 97US-0846247.
XX PR 06-MAY-1998; 98US-0073538.
XX PR 28-AUG-1998; 98US-0141908.
XX PA
XX PA (KOSA-) KOSAN BIOSCIENCES INC.
XX PI
XX PI Ashley G, Betlach MC, Betlach M, Tang L, McDaniel R;
XX DR
XX DR WPI: 2000-610844/58.
XX PT
XX PT New recombinant pick hydroxylase gene of Streptomyces venezuelae useful
XX PT for converting ketolides to antibiotics and as antibiotics and
XX PT intermediates in the synthesis of compounds with pharmaceutical value
XX XX
XX PS Disclosure; Columns 39-40; 117pp; English.
XX XX
XX CC The present sequence represents a partial S-adenosylmethionine synthase.
XX CC The nucleotide sequence encoding it is used in the course of the
XX CC invention. The specification describes a recombinant DNA compound
XX CC expressing recombinant polyketide synthase genes in host cells for the
XX CC production of nardoniolide, nardoniolide derivatives and polyketides that
XX CC are useful as antibiotics and as intermediates in the synthesis of
XX CC compounds with pharmaceutical value. The DNA compounds may also encode
XX CC a C12-hydroxylase (pick), desosamine biosynthesis and desosaminyl
XX CC transferase enzymes (useful for conversion of ketolides to antibiotics),
XX CC and the beta-glucosidase enzyme (involved in picromycin biosynthesis).
XX CC These compounds are also useful for increasing the antibiotic activity
XX CC of a compound relative to the unhydroxylated compound. The recombinant
XX CC host cells are useful as genetic systems that allow rapid engineering
XX CC of the nardoniolide polyketide synthase. These would be valuable for
XX CC creating novel ketolide analogs for pharmaceutical applications.
XX XX
XX SQ Sequence 332 AA;
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alignment_scores:
    Quality: 70.00      Length: 20
    Ratio: 4.375      Gaps: 0
Percent Similarity: 80.000 Percent Identity: 65.000
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US-09-198-779B-1 x AAB18652 ..
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Align seg 1/1 to: AAB18652 from: 1 to: 332
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163 TTCTATCAAGACCGCGCATACGGCCACTTTGGCCGCTAGACGACGCGGCACTT 212
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299 TGTGCTGTTTATATATATATATATATATATATATATATATATATATATATATAT 315
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213 CACCTGGCAG 222
|||||
315 eThrTrrpGlu 318

seq_name: /SIDSI/gcgcdata/genesegp-emb1/AA2000.DAT:AA67216
seq_documentation_block:
ID AAY67216 standard; protein; 332 AA.
AC AAY67216;
XX XX
XX DT 23-MAR-2000 (first entry)
XX XX
XX DE ORF 15 encoded S-adenosylmethionine synthase (SAM synthase).
XX XX
XX KM Nardoniolide polyketide synthase; PKS; desosamine biosynthesis; ketolide;
XX KM SAM synthase; S-adenosylmethionine synthase; antibiotic production;
XX KM nardomycin; picromycin.
XX XX
XX OS Streptomyces venezuelae.
XX EN
XX EN WO961599-A2.
XX PD
XX PD 02-DEC-1999.
XX XX
XX PF 27-MAY-1999; 99WO-US11814.
XX XX
XX PR 28-MAY-1998; 98US-0087080.
XX PR 28-AUG-1998; 98US-0141908.
XX PR 22-SEP-1998; 98US-0100880.
XX PR 08-FEB-1999; 99US-0119139.
XX XX
XX PA (KOSA-) KOSAN BIOSCIENCES INC.
XX PI
XX PI Ashley G, Betlach MC, Betlach M, McDaniel R, Tang L;
XX DR
XX DR WPI: 2000-072618/06.
XX DR N-PSDB; AA256005.
XX XX
XX PT New recombinant DNA encoding a domain of nardoniolide polyketide
XX PT synthase, for production of ketolide antibiotics -
XX XX
XX PS Example 2; Page 33-34; 98pp; English.
XX XX
XX CC This is the Streptomyces venezuelae S-adenosylmethionine synthase, SAM
XX CC synthase amino acid sequence, encoded by ORF15. This protein is involved
XX CC in desosamine biosynthesis. The invention relates to recombinant DNA
XX CC containing a coding sequence for a nardoniolide polyketide synthase
XX CC (PKS). Polyketides are compounds synthesised from 2-carbon units through
XX CC a series of condensations and subsequent modifications. Modular PKSs are
XX CC responsible for the production of many antibiotics including picromycin.
XX CC The nardoniolide PKS consists of a loading module, six extender modules,
XX CC and two thioester domains. Four proteins make up the nardoniolide PKS
XX CC (PICAI, PICAIR, PICAIRI and PICAIIV). PICAI includes the loading module
XX CC and extender modules 1 and 2, PICAIRI includes extender modules 3 and 4,
XX CC PICAIIV includes extender module 5 and PICAIIV includes extender module 6
XX CC and a type II thioesterase domain. The second type II thioesterase
XX CC domain is found on the PICB protein. The nucleotide sequences encoding
XX CC all of these proteins can be isolated in recombinant form from the
XX CC recombinant cosmid PKOS023-27 (see AA256001). Nardoniolide is
XX CC desosaminylated in S. venezuelae to yield nardomycin, the desosaminyl
XX CC transferase enzyme is required for this conversion, and the desosamine
XX CC biosynthetic genes are also found in cosmid PKOS023-27. The recombinant
XX CC DNA of the invention is used to express, in transformed cells,
XX CC nardoniolide (or its derivatives) or other ketolides (particularly
XX CC hybrids), which may then be converted (e.g. by other enzymes
XX CC recombinantly expressed in the same hosts) to polyketide antibiotics or
XX CC their intermediates. The antibiotics are useful in human or veterinary
XX CC medicine.
XX XX
XX SQ Sequence 332 AA;
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## alignment\_scores:

Quality: 70.00 Length: 20  
Ratio: 4.375 Gaps: 0  
Percent Similarity: 80.000 Percent Identity: 65.000

## alignment\_block:

US-09-198-779b-1 x AAV67216 ..

Align seg 1/1 to: AAV67216 from: 1 to: 332

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299 TYSERGLTHRALAATYRGLYHISPHGLYARGGLULEUPROASPH 315

213 CACCTCGCAG 222

||| |||  
315 ethrrtprglu 318

seq\_name: /SIDSI/gcdata/geneseq/geneseqp-emb1/AA1994.DAT:AA54204

seq\_documentation\_block:

ID AAR54204 standard; Protein: 402 AA.

AC AAR54204;

DT 18-NOV-1994 (first entry)

DE snac gene product involved in streptogramin biosynthetic pathway.

XX Antibiotic; streptogramin; snac; snab; snac; biosynthesis; enzyme;  
KW biosynthetic pathway; Streptomyces pristinaespiralis.  
XX

OS Streptomyces pristinaespiralis.

PN FR696189-A.

PD 01-APR-1994.

PF 25-SEP-1992; 92FR-0011441.

PR 25-SEP-1992; 92FR-0011441.

PA (RHON ) RHONE POULENC RORER SA.

PI Blanc V, Blanche F, Crouzet J, Jacques N, Lacroix P;

PT Ribaut D, Zagorec M;

DR WPI: 1994-128286/16.  
N-PSDB; AAG64204.

XX DNA involved in streptogramin antibiotic biosynthesis - for  
PT prodn. or bio-conversion of streptogramin(s) or prodn. of  
PT streptogramin intermediates, derivs. or hybrid antibiotics  
PS Claim 21, Page 55-57; 83pp; French.

XX The snac gene product is involved in the biosynthesis of  
CC streptogramins, antibiotics active against Gram positive bacteria.  
CC The identification of the sequences encoding the enzymes involved  
CC in the biosynthetic pathway means that they can be isolated and  
CC manipulated. Mutant microorganisms in which a step in the  
CC streptogramin biosynthetic pathway is blocked can be cultured to  
CC produce streptogramin intermediates, which may later be converted  
CC to streptogramin derivatives. Recombinant cells may also be used  
CC for the bioconversion of streptogramins from one form to another or  
CC for the production of hybrid antibiotics.  
SQ

Sequence 402 AA;

alignment\_scores:

Quality: 69.00

Length: 20

Ratio: 4.600 Gaps: 0  
Percent Similarity: 75.000 Percent Identity: 65.000

alignment\_block:

US-09-198-779b-1 x AAR54204 ..

Align seg 1/1 to: AAR54204 from: 1 to: 402

163 TTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGACTT 212  
::: |||||  
369 TYRALAALATHRALAATYRGLYHISPHGLYARGGLULEUPROASPH 385

213 CACCTCGCAG 222

||| |||  
385 ethrrtprglu 388

seq\_name: /SIDSI/gcdata/geneseq/geneseqp-emb1/AA2001.DAT:AAU71922

seq\_documentation\_block:

ID AAU71922 standard; Protein: 407 AA.

AC AAU71922;

DT 26-FEB-2002 (first entry)

DE C. glutamicum metabolic pathway protein encoded by gene #57.

XX Metabolic pathway protein; MP; lysine biosynthesis pathway;  
KW methionine biosynthesis pathway; large-scale production of fine chemical;  
KW Corynebacterium diptheriae; diptheria.

XX Corynebacterium glutamicum.

PN W0200166573-A2.

PD 13-SEP-2001.

PF 22-DEC-2000; 2000WO-IB02035.

PR 09-MAR-2000; 2000US-187970P.

PR 23-JUN-2000; 2000US-0606740.

PA (BADI ) BASF AG.

PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G, Kim J;

PT Lee H, Hwang B;

DR WPI: 2001-582269/65.  
N-PSDB; AAS96132.

XX Nucleic acids encoding metabolic pathway proteins from Corynebacterium  
PT glutamicum, useful for producing methionine and lysine in  
PT Corynebacterium and Brevibacterium -  
PS Disclosure; Page 311-312; 316pp; English.

XX The present invention relates to the isolation of novel Corynebacterium  
CC glutamicum genes (AAS96073-AAS96132) encoding metabolic pathway (MP)  
CC proteins. The metabolic pathway proteins of the invention  
CC include enzymes involved in the lysine and methionine biosynthetic  
CC pathways. The polynucleotide sequences of the invention can be used  
CC for the large-scale production and/or modulation of expression of the  
CC fine chemicals such as lysine and methionine. The sequences of the  
CC invention may be used to identify C. glutamicum and related organisms  
CC e.g. C. diptheriae in a subject to detect diptheria.  
CC AAU71863-AAU71922 represent the novel C. glutamicum metabolic pathway  
CC proteins of the invention.  
SQ

Sequence 407 AA;

alignment\_scores:

Quality: 67.00

Length: 22

Ratio: 4.188 Gaps: 0  
Percent Similarity: 72.727 Percent Identity: 54.545

Alignment\_block:

US-09-198-779B-1 x AAU71922 ..

Align seg 1/1 to: AAU71922 from: 1 to: 407

```
163 TTTCATCAAGACGGCGCATACGGCCACTTGGCGGTGACGACGCGGACTT 212
    ::::::::::::::::::::::::::::::::::::|||:::
373 TyrAlaAspThrAlaAlaIaTyrGlyHisPheGlyArgThrAspLeuAspLe 389
    :|:::
213 CACCTGCGAGGTGTC 228
    :|:::
389 uProTPrGluaIaile 394
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seq\_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AA691519

seq\_documentation\_block:

ID AAG91519 standard: Protein; 407 AA.

AC AAG91519;

DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 5273.

KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KM organic acid synthesis.

OS Corynebacterium glutamicum.

PN EP1108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

PR 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

DR WPI; 2001-376931/40.

DR N-PSDB; AAH66738.

XX

PT Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene

PT

XX

PS Claim 17; SEQ ID NO: 5273; 246pp + Sequence Listing; English.

XX

CC The present invention provides a number of nucleotide and protein

CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

CC are useful for identifying the mutation point of a gene derived from a

CC mutant of coryneform bacterium, measuring expression amount and

CC analysing the expression profile or expression pattern of a gene derived

CC from Coryneform bacterium, and identifying a homologue of a gene derived

CC from coryneform bacterium. Coryneform bacteria are useful for producing

CC amino acids, nucleic acids, vitamins, saccharides and organic acids,

CC particularly L-lysine. The present sequence is a protein described

CC in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the

CC

XX

Sequence 407 AA;

alignment\_scores:

Quality: 67.00

Ratio: 4.188

Percent Similarity: 72.727

Percent Identity: 54.545

Alignment\_block:

US-09-198-779B-1 x AAG91519 ..

Align seg 1/1 to: AAG91519 from: 1 to: 407

```
163 TTTCATCAAGACGGCGCATACGGCCACTTGGCGGTGACGACGCGGACTT 212
    ::::::::::::::::::::::::::::::::::::|||:::
373 TyrAlaAspThrAlaAlaIaTyrGlyHisPheGlyArgThrAspLeuAspLe 389
    :|:::
213 CACCTGCGAGGTGTC 228
    :|:::
389 uProTPrGluaIaile 394
```

seq\_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAB79754

seq\_documentation\_block:

ID AAB79754 standard: Protein; 407 AA.

AC AAB79754;

DT 30-APR-2001 (first entry)

DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:242.

KW fine chemical production; microorganism; organic acid; nucleoside;

KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;

KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;

KW carbohydrate; aromatic compound; cofactor; polypeptide; enzyme.

XX

OS Corynebacterium glutamicum.

PN WO200100843-A2.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-IB00923.

PR 25-JUN-1999; 99US-0141031.

PR 01-JUL-1999; 99DE-1030476.

PR 02-JUL-1999; 99US-0142101.

PR 08-JUL-1999; 99DE-1031415.

PR 08-JUL-1999; 99DE-1031418.

PR 08-JUL-1999; 99DE-1031419.

PR 08-JUL-1999; 99DE-1031420.

PR 08-JUL-1999; 99DE-1031424.

PR 08-JUL-1999; 99DE-1031428.

PR 08-JUL-1999; 99DE-1031434.

PR 08-JUL-1999; 99DE-1031435.

PR 08-JUL-1999; 99DE-1031443.

PR 08-JUL-1999; 99DE-1031453.

PR 08-JUL-1999; 99DE-1031457.

PR 08-JUL-1999; 99DE-1031465.

PR 08-JUL-1999; 99DE-1031478.

PR 08-JUL-1999; 99DE-1031510.

PR 08-JUL-1999; 99DE-1031541.

PR 08-JUL-1999; 99DE-1031573.

PR 08-JUL-1999; 99DE-1031582.

PR 08-JUL-1999; 99DE-1031632.

PR 08-JUL-1999; 99DE-1031634.

PR 08-JUL-1999; 99DE-1031636.

PR 09-JUL-1999; 99DE-1032125.

PR 09-JUL-1999; 99DE-1032126.

PR 09-JUL-1999; 99DE-1032130.

PR 09-JUL-1999; 99DE-1032186.

PR 09-JUL-1999; 99DE-1032206.

PR 09-JUL-1999; 99DE-1032227.

```
PR 09-JUL-1999; 99DE-1032228.
PR 09-JUL-1999; 99DE-1032229.
PR 09-JUL-1999; 99DE-1032230.
PR 14-JUL-1999; 99DE-1032922.
PR 14-JUL-1999; 99DE-1032926.
PR 14-JUL-1999; 99DE-1032928.
PR 14-JUL-1999; 99DE-1033004.
PR 14-JUL-1999; 99DE-1033005.
PR 14-JUL-1999; 99DE-1033006.
PR 12-AUG-1999; 99DE-1033006.
PR 12-AUG-1999; 99DE-1033006.
PR 27-AUG-1999; 99DE-1040764.
PR 27-AUG-1999; 99DE-1040765.
PR 27-AUG-1999; 99DE-1040766.
PR 27-AUG-1999; 99DE-1040832.
PR 31-AUG-1999; 99DE-1041378.
PR 31-AUG-1999; 99DE-1041379.
PR 31-AUG-1999; 99DE-1041380.
PR 31-AUG-1999; 99DE-1041394.
PR 31-AUG-1999; 99DE-1041396.
PR 03-SEP-1999; 99DE-1042076.
PR 03-SEP-1999; 99DE-1042077.
PR 03-SEP-1999; 99DE-1042079.
PR 03-SEP-1999; 99DE-1042086.
PR 03-SEP-1999; 99DE-1042087.
PR 03-SEP-1999; 99DE-1042088.
PR 03-SEP-1999; 99DE-1042095.
PR 03-SEP-1999; 99DE-1042124.
PR 03-SEP-1999; 99DE-1042129.
PR 09-MAR-2000; 2000US-0187970.
XX
XX (BAD1 ) BASF AG.
XX
XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
XX WPI; 2001-137957/14.
XX N-PSDB; AAF71873.
XX
XX Nucleic acids from Corynebacterium glutamicum encoding metabolic
XX pathway proteins, useful for producing fine chemicals in
XX microorganisms, including organic acids, nonproteinogenic amino acids,
XX and purine and pyrimidine bases -
XX
XX Claim 20; Page 509-511; 1737pp; English.
XX
XX AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
XX pathway (WP) proteins given in AAB79634 to AAB80211. The C. glutamicum
XX MP nucleic acids are useful for the production of fine chemicals
XX in microorganisms, including organic acids, nonproteinogenic amino
XX acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
XX saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
XX compounds, vitamins, cofactors, polyketides and enzymes.
XX
XX Sequence 407 AA:
SQ
alignment_scores:
Quality: 67.00 Length: 22
Ratio: 4.188 Gaps: 0
Percent Similarity: 72.727 Percent Identity: 54.545
alignment_block:
US-09-198-779b-1 x AAB79754 ..
Align seg 1/1 to: AAB79754 from: 1 to: 407
163 TTCATCAAGACCGCGCATAGCGCCACTTGGCCGAGACGCGGACATT 212
::: ||||||||||||||||||||||||| ||| |||::
373 TTTAAlAspThrAlaIatYrGlyHisPheGlyArgThrAspLeuAsp 389
213 CACCTGCGAGGTGTC 228
: |||:::
389 uProTrpGluAlaIle 394
```

```
seq_name: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1995.DAT: AAR80060
seq_documentation_block:
ID AAR80060 standard; Protein; 412 AA.
XX
XX AAR80060;
XX
XX 26-APR-1996 (first entry)
XX
XX S-adenosylmethionine synthetase.
XX
XX Coryneform bacteria; S-adenosylmethionine synthetase; production: ss.
XX
XX Brevibacterium flavum strain MJ-233.
XX
XX JP07227287-A.
XX
XX 29-AUG-1995.
XX
XX 18-FEB-1994; 94JP-0020809.
XX
XX 18-FEB-1994; 94JP-0020809.
XX
XX (MITU ) MITSUBISHI CHEM CORP.
XX
XX WPI; 1995-331524/43.
XX N-PSDB; AAT04566.
XX
XX DNA encoding S-adenosylmethionine synthetase - useful for the
XX efficient production of the enzyme
XX
XX Claim 4; Page 5-7; 7pp; Japanese.
XX
XX The S-adenosylmethionine synthetase is derived from a Coryneform
XX bacterium. The DNA encoding it (AAT04566) is used to transform bacteria
XX to efficiently produce the enzyme. A 5.5 kb Sali DNA fragment contg.
XX this DNA gives fragments of 2.4, 1.7 and 1.4 kb when cleaved with
XX BamHI and fragments of 3.3, 1.0, 0.7 and 0.5 kb when cleaved with PstI.
XX
XX Sequence 412 AA:
SQ
alignment_scores:
Quality: 67.00 Length: 22
Ratio: 4.188 Gaps: 0
Percent Similarity: 72.727 Percent Identity: 54.545
alignment_block:
US-09-198-779b-1 x AAR80060 ..
Align seg 1/1 to: AAR80060 from: 1 to: 412
163 TTCATCAAGACCGCGCATAGCGCCACTTGGCCGAGACGCGGACATT 212
::: ||||||||||||||||||||||||| ||| |||::
374 TTTAAlAspThrAlaIatYrGlyHisPheGlyArgThrAspLeuAsp 390
213 CACCTGCGAGGTGTC 228
: |||:::
390 uProTrpGluAlaIle 395
seq_name: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA2001.DAT: ABB52815
seq_documentation_block:
ID ABB52815 standard; Protein; 383 AA.
XX
XX ABB52815;
XX
XX 11-FEB-2002 (first entry)
XX
XX Escherichia coli polypeptide SEQ ID NO 1033.
XX
XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
XX immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
XX
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XX  antibiotic; antibacterial; drug design.
XX  Enterococcus faecalis.
XX  WO200170955-A2.
XX  27-SEP-2001.
XX  21-MAR-2001; 2001WO-US09180.
XX  21-MAR-2000; 2000US-191078P.
XX  23-MAY-2000; 2000US-206848P.
XX  26-MAY-2000; 2000US-207727P.
XX  23-OCT-2000; 2000US-242578P.
XX  27-NOV-2000; 2000US-253625P.
XX  22-DEC-2000; 2000US-257931P.
XX  16-FEB-2001; 2001US-269308P.
XX  (ELIT-) ELITRA PHARM INC.
XX  Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX  Yamamoto RT, Xu HH;
XX  WPI; 2001-611495/70.
XX  N-PSDB; AAS5124I.
XX  New polynucleotides for the identification and development of
XX  antibiotics, comprise sequences of antisense nucleic acids -
XX  Example 3; Seq ID No 4878; 511pp; English.
XX  The invention relates to antisense inhibitors of genes essential to
XX  prokaryotic cellular proliferation, their use in identifying the
XX  genes, their use in the discovery of novel antibiotics, the essential
XX  genes themselves and the encoded proteins. The prokaryotes used are
XX  Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX  pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX  invention is also useful for the identification of potential new targets
XX  for antibiotic development. The antisense nucleic acids can also be used
XX  to identify proteins used in proliferation, to express these proteins,
XX  and to obtain antibodies capable of binding to the expressed proteins.
XX  The proteins can be used to screen compounds in rational drug discovery
XX  programmes. The antisense nucleic acid sequence is also useful to screen
XX  for homologous nucleic acids which are required for cell proliferation in
XX  a wide variety of organisms. The present sequence represents an
XX  essential prokaryotic cellular proliferation protein.
XX  Note: The sequence data for this patent did not form part
XX  of the printed specification, but was obtained in electronic
XX  format directly from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences.
XX  Sequence 386 AA;
XX
XX  Alignment_scores:
XX      Quality: 64.00      Length: 18
XX      Ratio: 4.571      Gaps: 0
XX  Percent Similarity: 77.778      Percent Identity: 66.667
XX
XX  alignment_block:
XX  US-09-198-779B-1 x AAU33382 ..
XX
XX  Align seg 1/1 to: AAU33382 from: 1 to: 386
XX
XX  169 AAGACCGCGCATACGGCCATTGGCGGTGACAGCGCCGACTTCACCTG 218
XX  ::::::::::::::::::::::::::::||| |||:::
XX  360 GlntrAlaAlaIatYrcG1YhtSPheG1yArGtrnAspIleAspIeuProtr 376
XX
XX  219 CGAG 222
XX  |||
XX  376 pcIu 377

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Align seg 11 to: AAU35173 from: 1 to: 394  
 169 AAGACGGCGGCAATAGCGACACTTTGGCCGTGACGACGCCGACTTCACCTG 218  
 :::  
 363 GINTThraAlaAtyTcLYHisPheGlyArGTrhAspIleAspLeuProTr 379  
 219 CGAG 222  
 |||  
 379 pGlu 380  
 seq\_name: /SIDS1/gcgcdata/geneseq/geneseqp-emb1/AA2001.DAT:ABG25556  
 seq\_documentation\_block:  
 ID ABG25556 standard; Protein: 94 AA.  
 XX  
 AC ABG25556;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #25547.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX food supplement; medical imaging; diagnostic; genetic disorder.  
 OS Homo sapiens.  
 XX  
 WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 XX 23-AUG-2000; 2000US-0549167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Dermanac RT, Liu C, Tang YF.  
 XX  
 DR WPI; 2001-639362/73.  
 XX  
 DR N-PSDB; AAS89743.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX  
 PS Claim 20; SEQ ID No 55915; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at fcp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 Q0 Sequence 94 AA;



alignment\_scores:                   Quality:   63.00                   Length:   55  
                                  Ratio:   2.100                   Gaps:   1  
Percent Similarity: 54.545           Percent Identity: 32.727

alignment\_block:  
US-09-198-779B-1/rev x ABG25556 ..

Align seg 1/1 to: ABG25556 from: 1 to: 94

226 CCACCTCCGACGAGTGAAGTCGGCGGTGCATCAATTAACATTAATACAC 177  
    |||   |||   |||   |||   |||   |||   |||   |||   |||   |||  
12 ProAlaArgProGlnSerArgLeuAlaHisArgGlnArgGlyArgMetAr 28

176 GCGGCTTGATGAACCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 127  
    |   |||   :::   |||                                   :::  
28 g.GlyAlaProArgProPheArgGlnArgGlnIleLysLeuCySTyrAla 44

126 NNNNNAAGTACGTGTGTGTCCTGTCATTAATTAACATTAATACAC 77  
    |||   :::   |||   |||   |||   |||   |||   |||   |||   |||  
45 ArgCysThrProThrIleCysProThrIlySerArgSerArSnth 61

76 AAGCAACATGCA 64  
    |:::   :::   |||  
61 rValThrSerGly 65

seq\_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:ABG22853

seq\_documentation\_block:  
ID ABG22853 standard; Protein: 398 AA.

XX AC ABG22853;  
XX DT 18-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #22844.  
XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI: 2001-639362/73.  
XX DR N-PSDB: AAS87040.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity -  
XX PS Claim 20: SEQ ID No 53212; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and  
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX CC and gene mapping, and in recombinant production of (II). The  
XX CC polynucleotides are also used in diagnostics as expressed sequence tags  
XX CC for identifying expressed genes. (II) is useful in gene therapy techniques  
XX CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 398 AA;

alignment\_scores:                   Quality:   63.00                   Length:   21  
                                  Ratio:   3.938                   Gaps:   1  
Percent Similarity: 76.190           Percent Identity: 66.667

alignment\_block:  
US-09-198-779B-1 x ABG22853 ..

Align seg 1/1 to: ABG22853 from: 1 to: 398

169 AAGACCGCCGATPACGCCACTTTGGCGGTGACGACGCCGACTTCACTG 218  
    :::   |||   |||   |||   |||   |||   |||   |||   |||   |||  
376 ArgTrnAlaAlaIlyrGlyHisPheGlyArgAsp.....SerPheProTr 390

219 CGAGGTGTCAG 231  
    |||   |||   |||  
390 pGluValProLys 394

seq\_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:AAW20562

seq\_documentation\_block:  
ID AAW20562 standard; Protein: 104 AA.

XX AC AAW20562;  
XX DT 17-JUL-1997 (first entry)  
XX DE H. pylori cytoplasmic protein 677088.aa.  
XX KW Cytoplasmic; vaccine; prevention; infection; identification;  
XX KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;  
XX KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.  
XX OS Helicobacter pylori.  
XX PN WO9640893-A1.  
XX PD 19-DEC-1996.  
XX PF 06-JUN-1996; 96WO-US09122.  
XX PR 01-APR-1996; 96US-0630405.  
XX PR 07-JUN-1995; 95US-0487032.  
XX PA (ASTR ) ASTRA AB.  
XX PI Berglindh OT, Smith D, Melligaard BL;  
XX DR WPI: 1997-052306/05.  
XX DR N-PSDB: AAT67709.  
XX PT Helicobacter pylori nucleic acid sequences and related  
XX PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori  
XX PT infection, and to detect Helicobacter

PI Alm RA, Smith D;

PD 19-DEC-1996.

```

XX 06-JUN-1996; 96WO-US09122.
PF
XX
PR 01-APR-1996; 96US-0630405.
PR 07-JUN-1995; 95US-0487032.
XX
XX (ASTR ) ASTRA AB.
XX
PI Berglinde OT, Smith D, Mellgaard BL;
XX
XX WPI, 1997-052306/05.
DR
DR N-PSDB; AAT68254.
XX
XX
XX Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
XX
XX
XX Claim 61; Page 1392; 1481pp; English.
PS
XX
XX The present sequence is a H. pylori cytoplasmic protein involved in
CC nucleotide metabolism.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
XX production, e.g. in E. coli hosts.
XX
SQ Sequence 253 AA;

```

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alignment_scores:
  Quality: 61.00      Length: 17
  Ratio: 4.357      Gaps: 0
  Percent Similarity: 82.353      Percent Identity: 64.706

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alignment_block:
US-09-198-779B-1 x AAW21001 ..

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Align seg 1/1 to: AAW21001 from: 1 to: 253

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172 ACCGCCGATACGGCACTTGGCGTGACGACGCCGACTTCACCTGCCA 221
||||:|||||||||||||||||:|||||:|||||
223 ThrSerAlaIyrGlyHisPheGlyArgGluLeuGluInuPheThrTrpG1 239
222 G 222
|
239 u 239

```

**THIS PAGE BLANK (USPTO)**



APPLICANT: BETLACH, Mary C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
FILE REFERENCE: 300622002120  
CURRENT APPLICATION NUMBER: US/09/320,878A  
EARLIER FILING DATE: 1999-05-27  
EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
EARLIER FILING DATE: 1998-08-28  
EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
EARLIER FILING DATE: 1998-05-06  
EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: 60/119,139  
EARLIER FILING DATE: 1999-02-08  
EARLIER APPLICATION NUMBER: 60/100,880  
EARLIER FILING DATE: 1998-09-22  
EARLIER APPLICATION NUMBER: 60/087,080  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 332  
TYPE: PRT  
ORGANISM: Streptomyces venezuelae  
US-09-320-878-16

alignment\_scores:  
Quality: 70.00 Length: 20  
Ratio: 4.375 Gaps: 0  
Percent Similarity: 80.000 Percent Identity: 65.000

## alignment\_block:

US-09-198-779b-1 x US-09-320-878-16 ..

Align seg 1/1 to: US-09-320-878-16 from: 1 to: 332

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::: |||||||||||||||||||||||||||||  
299 TYRSGELHTRALALATYRGLYHISPNEGLYARGGLULEUPROASPH 315  
213 CACCTGCGAG 222  
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315 ETHRTTRPGLU 318

seq\_name: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:US-08-403-852D-19

## seq\_documentation\_block:

Sequence 19, Application US/08403852D  
Patent No. 5891695  
GENERAL INFORMATION:  
APPLICANT: Blanc, Veronique  
APPLICANT: Blanche, Francis  
APPLICANT: Crouzet, Joel  
APPLICANT: Jacques, Nathalie  
APPLICANT: Lacroix, Patricia  
APPLICANT: Thibaut, Denis  
APPLICANT: Zagorec, Monique  
APPLICANT: Debussche, Laurent  
TITLE OF INVENTION: Polypeptides Involved In The  
Biosynthesis Of Streptogramins, Nucleotide Sequences  
TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,852D  
FILING DATE: 10-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR 93/00923  
FILING DATE: 25-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92/11441  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03806,0054-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 402 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-403-852D-19

alignment\_scores:  
Quality: 69.00 Length: 20  
Ratio: 4.600 Gaps: 0  
Percent Similarity: 75.000 Percent Identity: 65.000

## alignment\_block:

US-09-198-779b-1 x US-08-403-852D-19 ..

Align seg 1/1 to: US-08-403-852D-19 from: 1 to: 402

163 TTCATCAGACCGCGCATACGCGCACTTGGCCGTGACGACCGCCACTT 212  
::: |||||||||||||||||||||||||||||  
369 TYRALALATHTRALALATYRGLYHISPNEGLYARGGLULEUPROASPH 385  
213 CACCTGCGAG 222  
||| |||  
385 ETHRTTRPGLU 388

seq\_name: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:US-08-510-646B-20

## seq\_documentation\_block:

Sequence 20, Application US/08510646B  
Patent No. 6077699  
GENERAL INFORMATION:  
APPLICANT: Blanc, Veronique  
APPLICANT: Blanche, Francis  
APPLICANT: Crouzet, Joel  
APPLICANT: Jacques, Nathalie  
APPLICANT: Lacroix, Patricia  
APPLICANT: Thibaut, Denis  
APPLICANT: Zagorec, Monique  
APPLICANT: Debussche, Laurent  
TITLE OF INVENTION: Polypeptides Involved In The  
Biosynthesis Of Streptogramins, Nucleotide Sequences  
TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-510-646B-20

alignment_scores:
Quality: 69.00 Length: 20
Ratio: 4.600 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 65.000

alignment_block:
US-09-198-779B-1 x US-08-510-646B-20 ..

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163 TTCATCAAGACCGCCGATAGCGCCACTTTGGCGGTACGACGCGGACTT 212
::: ||||||||||||||||||||||||||||| |||||
369 TyrAlaAlaThrAlaAlaTyrGlyHisPheGlyArgGluLeuProAspPh 385
213 CACCTGGGAG 222
|||||
385 ethrTrpGlu 388

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-09-231-818-19

seq_documentation_block:
; Sequence 19, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Bianche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
```

```
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-231-818-19

alignment_scores:
Quality: 69.00 Length: 20
Ratio: 4.600 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 65.000

alignment_block:
US-09-198-779B-1 x US-09-231-818-19 ..

Align seg 1/1 to: US-09-231-818-19 from: 1 to: 402
163 TTCATCAAGACCGCCGATAGCGCCACTTTGGCGGTACGACGCGGACTT 212
::: ||||||||||||||||||||||||||||| |||||
369 TyrAlaAlaThrAlaAlaTyrGlyHisPheGlyArgGluLeuProAspPh 385
213 CACCTGGGAG 222
|||||
385 ethrTrpGlu 388

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-339-152A-21

seq_documentation_block:
; Sequence 21, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/339,152A  
FILING DATE: 10-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 0609,4120000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-339-152A-21

alignment\_scores:  
Quality: 55.50 Length: 19  
Ratio: 3.469 Gaps: 1  
Percent Similarity: 84.211 Percent Identity: 63.158

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US-09-198-779b-1/rev x US-08-339-152A-21 ..

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22 ThrAlaGlnValGlnAlaAlaSerSer...ProArgTrpProGlnIleal 37

174 GGTCTTG 168  
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seq\_documentation\_block:

Sequence 12, Application US/08007999B

Patent No 5851787

GENERAL INFORMATION:

APPLICANT: Masco, Wilma

APPLICANT: Bupp, Keith

APPLICANT: Magendantz, Margaret

APPLICANT: Tanzl, Rudolph

TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/007,999B

FILING DATE: 21-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,642  
FILING DATE: 20-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/930,022  
FILING DATE: 17-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, G. Kevin  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: 0609,3520002/JAG/GKT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2571  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-007-999B-12

alignment\_scores:  
Quality: 55.50 Length: 19  
Ratio: 3.469 Gaps: 1  
Percent Similarity: 84.211 Percent Identity: 63.158

alignment\_block:  
US-09-198-779b-1/rev x US-08-007-999B-12 ..

Align seg 1/1 to: US-08-007-999B-12 from: 1 to: 197

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174 GGTCTTG 168  
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37 aValleu 39

seq\_name: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep:US-08-689-276A-12

seq\_documentation\_block:

Sequence 12, Application US/08689276A

Patent No 589191

GENERAL INFORMATION:

APPLICANT: Masco, Wilma

APPLICANT: Bupp, Keith

APPLICANT: Magendantz, Margaret

APPLICANT: Tanzl, Rudolph

TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave., NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/689,276A

FILING DATE: 06-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/007,999

FILING DATE: 21-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,642

FILING DATE: 20-APR-1992







APPLICATION NUMBER: 08/7229.743

REGISTRATION NUMBER: 36,627

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 966 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-571-758-2

alignment\_scores:  
Quality: 53.00 Length: 39  
Ratio: 2.304 Gaps: 1  
Percent Similarity: 58.974 Percent Identity: 35.897

alignment\_block:  
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71 A.....CAATGATCAGACCGCTCCATTATCAGACATGGCAGCGTCGA 28
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103 uLeuArgGlnIleuArgValGlyLeuSerGlnGlyThrLeuThra 120
27 TCTGTCACGCGGCTA 11
||| |||||
120 lacysLeuAlaArgLeu 125
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Fax: 515-294-2299  
Email: schnable@iastate.edu  
Primer A: TATACCATCACTTAAGCCG  
Primer B: GAGACTTCGACTTCAGCC  
PCR Profile:

Denaturation: 94 degrees C for 30 seconds  
Annealing: 60 degrees C for 45 seconds  
Polymerization: 72 degrees C for 90 seconds  
PCR cycles: 31  
Thermal cycler: Perkin Elmer TC

## Protocol:

Template: 10-20 ng  
Primer: each 0.5 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/uL  
Total vol: 20 uL

## Buffer:

MgCl<sub>2</sub>: 2 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.4.

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/clone\_id="maize leaf DNA"  
/note="PCR products amplified from genomic DNA"  
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Query Match  
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Matches 73; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 159 caggttctcaagaccgcgcatacgcgcacttggccgtgacgagcgcgacttcaactg 218  
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DB 276 CAGGTTCAATCAAGACCGCGCTACGGCCACTTGGCGGTGACGACGCGGACTTCACCTG 217

QY 219 cgaagtgtcaagcccc 235  
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DB 216 GGAGTGTGTGAAGCCCC 200

RESULT 2  
G71468/c 319 bp DNA linear STS 08-JUN-2001  
LOCUS  
DEFINITION A60033234FM017 maize leaf DNA Zea mays STS genomic, sequence tagged  
site.  
G71468  
VERSION G71468.1 GI:14333153  
KEYWORDS  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
1 (bases 1 to 319)  
Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.  
3' UTR sequences of maize genes  
Unpublished

CONTACT: Schnable, P.S.  
Schnable Laboratory  
Iowa State University  
GA05 Agronomy Hall, Ames, IA 50011, USA  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu  
Primer A: TATACCATCACTTAAGCCG

Primer B: GAGACTTCGACTTCAGCC  
PCR Profile:

Denaturation: 94 degrees C for 30 seconds  
Annealing: 60 degrees C for 45 seconds  
Polymerization: 72 degrees C for 90 seconds  
PCR cycles: 31  
Thermal cycler: Perkin Elmer TC

## Protocol:

Template: 10-20 ng  
Primer: each 0.5 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/uL  
Total vol: 20 uL

## Buffer:

MgCl<sub>2</sub>: 2 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.4.

FEATURES  
source

Location/Qualifiers  
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/organism="Zea mays"  
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Matches 72; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 159 caggttctcaagaccgcgcatacgcgcacttggccgtgacgagcgcgacttcaactg 218  
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DB 282 CAGGTTCAATCAAGACCGCGCTACGGCCACTTGGCGGTGACGACGCGGACTTCACCTG 223

QY 219 cgaagtgtcaagcccc 235  
|||||  
DB 222 GGAGTGTGTGAAGCCCC 206

RESULT 3  
E14404 1182 bp DNA linear PAT 28-JUL-1999  
LOCUS  
DEFINITION cDNA encoding S-adenosylmethionine synthetase.  
E14404  
VERSION E14404.1 GI:5709087  
KEYWORDS JP 1997313186-A/3.  
SOURCE Hordeum vulgare.  
ORGANISM Hordeum vulgare.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
1 (bases 1 to 1182)  
Mori, S.  
GENE OF S-ADENOSYLMETHIONINE SYNTHASE  
Patent: JP 1997313186-A 3 09-DEC-1997;  
NIPPON OIL CO LTD  
OS Hordeum vulgare  
PN JP 1997313186-A/3  
PD 09-DEC-1997  
PE 28-MAY-1996 JP 1996133406  
PI MORI SATOSHI  
PC C12N15/09,C07H21/04,C12N9/00//A01H1/00,A01H5/00; CC  
Strandedness: Double;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
FH key Location/Qualifiers

CONTACT: Schnable, P.S.  
Schnable Laboratory  
Iowa State University  
GA05 Agronomy Hall, Ames, IA 50011, USA  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu  
Primer A: TATACCATCACTTAAGCCG

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 23:17:31 ; Search time 1925.22 Seconds

(without alignments)  
2554.376 Million cell updates/sec

Title: US-09-198-779B-1

Perfect score: 235

Sequence: 1 gtttcgcgtcagctcgtt.....ctgcgagtgctcagcccc 235

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_pn: \*  
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9: gb\_pr: \*  
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11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vi: \*  
30: em\_htcg\_hum: \*  
31: em\_htcg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match Length	ID	Description
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C	1	70.6	30.0	305	11	G70767	G70767 A6003234FB
C	2	69	29.4	319	11	G71468	G71468 A6003334FM
C	3	61.6	26.2	1182	6	E14404	E14404 cDNA encodi
C	4	61	26.0	1182	6	E14402	E14402 cDNA encodi
C	5	61	26.0	1353	8	BLXSNS	D63835 Barley mRNA
C	6	59.4	25.3	1182	6	E14403	E14403 cDNA encodi
C	7	56.2	23.9	1566	8	AF420238	AF420238 Dendrobu
C	8	56.2	23.9	1736	8	OSU82833	OSU82833 Oryza sativ
C	9	56.2	23.9	15064	2	AP003211	AP003211 Oryza sat
C	10	54.6	23.2	545	8	AY039010	AY039010 Elaeis ol
C	11	54.6	23.2	1272	8	ACU17241	U17241 Actinidia c
C	12	54.6	23.2	1437	8	POPSMDDPT	M73430 Populus x g
C	13	51.6	22.0	1628	8	MCU79767	U79767 Mesembryant
C	14	51.4	21.9	1547	8	AF004317	AF004317 Musa acum
C	15	51.4	21.9	1659	8	AB062358	AB062358 Phaseolus
C	16	51.2	21.8	1632	8	DINCARAA	M1882 D. carophyll
C	17	51	21.7	1594	8	OSA296743	AJ296743 Oryza sat
C	18	51	21.7	2183	8	OSASMS1	Z26867 O. sativa (P
C	19	51	21.7	150954	2	AC087552	AC087552 Oryza sat
C	20	50.4	21.4	1107	8	AY061895	AY061895 Arabidops
C	21	50.4	21.4	1440	8	AF428440	AF428440 Arabidops
C	22	50.4	21.4	1459	8	AY052311	AY052311 Arabidops
C	23	50.4	21.4	1508	8	AF325061	AF325061 Arabidops
C	24	50.4	21.4	1510	8	AY037214	AY037214 Arabidops
C	25	50.4	21.4	80167	8	AB022216	AB022216 Arabidops
C	26	50.4	21.4	121668	8	AC022521	AC022521 Arabidops
C	27	49.8	21.2	1539	8	AF170798	AF170798 Petunia x
C	28	49.8	21.2	1665	8	AF367310	AF367310 Arabidops
C	29	49.8	21.2	114950	8	AC006922	AC006922 Arabidops
C	30	48.8	20.8	772	8	AF443869	AF443869 Solanum t
C	31	48.8	20.8	1479	8	LESALMSGA	Z24741 L. esculentu
C	32	48.8	20.8	1534	8	CRSAMS1	Z71271 C. roseus mR
C	33	48.8	20.8	2559	8	ATSHSAM	M55077 A. thaliana
C	34	48.8	20.8	2559	8	ATSAMIGEN	X53323 A. thaliana
C	35	48.2	20.5	1173	8	AF183891	AF183891 Petunia x
C	36	48.2	20.5	1327	8	PEABENSTNA	L36680 Pisum sativ
C	37	48.2	20.5	1446	8	PSSAMS1	X82076 P. sativum m
C	38	48.2	20.5	1455	8	LESALMSGC	Z24743 L. esculentu
C	39	48.2	20.5	1531	8	AF321001	AF321001 Suaeda ma
C	40	48.2	20.5	1565	8	PHSAM1	X82214 P. hybrida m
C	41	48.2	20.5	1627	8	AF346306	AF346306 Elaeagnus
C	42	48	20.4	585	8	PUMMSMS2A	M62757 Parsley S-a
C	43	47.2	20.1	4459	8	AF271220	AF271220 Brassica
C	44	47	20.0	820	8	AF008568	AF008568 Chlamydom
C	45	46.6	19.8	1572	8	AF346305	AF346305 Elaeagnus

## ALIGNMENTS

RESULT 1  
G70767/c 305 bp DNA linear STS 08-JUN-2001  
LOCUS A6003234FB73 maize leaf DNA Zea mays STS genomic, sequence tagged  
DEFINITION site.  
ACCESSION G70767  
VERSION G70767.1 GI:14332452  
KEYWORDS STS.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 305)  
AUTHORS Yang, Y.T., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.  
TITLE 3' UTR sequences of maize genes  
JOURNAL Unpublished  
COMMENT

Contact: Schnable, P.S.  
Schnable Laboratory  
Iowa State University  
G405 Agronomy Hall, Ames, IA 50011, USA  
Tel: 515-294-0975



US-09-791-537-120897

alignment\_scores:

Quality: 118.00 Length: 25  
Ratio: 5.130 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779B-1 x US-09-791-537-120897 ..

Align seg 1/1 to: US-09-791-537-120897 from: 1 to: 394

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160 AGGTTTCATCAAGACCGCCGATACGGCCATTGGCCGTGACGAGCCGA 209
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362 ArgpheelletystrAlaAlaIatrglyHisPheglyArgGluAspProAs 378
210 CTTCACTGCGAGGTGTCAAGCCC 234
|||||
378 pPheThrTrpGluValValysPro 386

```

seq\_name: /cgn2\_6/prodata/2/paa/US09\_NEW\_COMB.pep:US-10-155-881-25460

seq\_documentation\_block:

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; Sequence 25460, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lotliya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 25460
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-155-881-25460

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alignment\_scores:

Quality: 118.00 Length: 25  
Ratio: 5.130 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779B-1 x US-10-155-881-25460 ..

Align seg 1/1 to: US-10-155-881-25460 from: 1 to: 436

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160 AGGTTTCATCAAGACCGCCGATACGGCCATTGGCCGTGACGAGCCGA 209
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404 ArgpheelletystrAlaAlaIatrglyHisPheglyArgGluAspProAs 420
210 CTTCACTGCGAGGTGTCAAGCCC 234
|||||
420 pPheThrTrpGluValValysPro 428

```

seq\_name: /cgn2\_6/prodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-111090

seq\_documentation\_block:

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; Sequence 111090, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210

```

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 111090

; LENGTH: 393

; TYPE: PRT

; ORGANISM: Musa acuminata

US-09-791-537-111090

alignment\_scores:

Quality: 117.00 Length: 25  
Ratio: 5.087 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 84.000

alignment\_block:

US-09-198-779B-1 x US-09-791-537-111090 ..

Align seg 1/1 to: US-09-791-537-111090 from: 1 to: 393

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160 AGGTTTCATCAAGACCGCCGATACGGCCATTGGCCGTGACGAGCCGA 209
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361 ArgYrleuLysThrAlaAlaIatrglyHisPheglyArgAspProAs 377
210 CTTCACTGCGAGGTGTCAAGCCC 234
|||||
377 pPheThrTrpGluValValysPro 385

```



361 ArgPheLeuLysThrAlaAlaIaTyrgLyHisPheGlyArgAspAspProAs 377  
210 CTTCACTCGAGGTGTCAGGCC 234  
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377 pPheHTrpGluValValIysPro 385

seq\_name: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-120900

seq\_documentation\_block:

; Sequence 120900, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 120900  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Catharanthus roseus  
US-09-791-537-120900

alignment\_scores:  
Quality: 120.00 Length: 25  
Ratio: 5.217 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779b-1 x US-09-791-537-120900 ..

Align seg 1/1 to: US-09-791-537-120900 from: 1 to: 393

160 AGGTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGAGAGCCGCA 209  
|||||:|||||  
361 ArgPheLeuLysThrAlaAlaIaTyrgLyHisPheGlyArgAspAspProAs 377  
210 CTTCACTCGAGGTGTCAGGCC 234  
||||| |||||||||  
377 pPheHTrpGluValValIysPro 385

seq\_name: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:US-10-155-881-37535

seq\_documentation\_block:

; Sequence 37535, Application US/10155881  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jindong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(15300)J  
; CURRENT APPLICATION NUMBER: US/10/155,881  
; CURRENT FILING DATE: 2002-05-22  
; NUMBER OF SEQ ID NOS: 37595  
; SEQ ID NO 37535  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-155-881-37535

alignment\_scores:  
Quality: 120.00 Length: 25  
Ratio: 5.217 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779b-1 x US-10-155-881-37535 ..

Align seg 1/1 to: US-10-155-881-37535 from: 1 to: 394

160 AGGTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGAGAGCCGCA 209  
|||||:|||||  
362 ArgPheLeuLysThrAlaAlaIaTyrgLyHisPheGlyArgAspAspProAs 378  
210 CTTCACTCGAGGTGTCAGGCC 234  
||||| |||||||||  
378 pPheHTrpGluValValIysPro 386

seq\_name: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-51046

seq\_documentation\_block:

; Sequence 51046, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 51046  
; LENGTH: 395  
; TYPE: PRT  
; ORGANISM: Populus deltoides  
US-09-791-537-51046

alignment\_scores:  
Quality: 120.00 Length: 25  
Ratio: 5.217 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779b-1 x US-09-791-537-51046 ..

Align seg 1/1 to: US-09-791-537-51046 from: 1 to: 395

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362 ArgPheLeuLysThrAlaAlaIaTyrgLyHisPheGlyArgAspAspProAs 378  
210 CTTCACTCGAGGTGTCAGGCC 234  
||||| |||||||||  
378 pPheHTrpGluValValIysPro 386

seq\_name: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-120897

seq\_documentation\_block:

; Sequence 120897, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 120897  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Oryza sativa

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; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6453
; LENGTH: 393
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-09-791-537-6453
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alignment_scores:
  Quality: 120.00      Length: 25
  Ratio: 5.217        Gaps: 0
  Percent Similarity: 92.000      Percent Identity: 88.000
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alignment_block:
US-09-198-779B-1 x US-09-791-537-6453 ..
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Align seg 1/1 to: US-09-791-537-6453 from: 1 to: 393
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361 ArgpheuLeuYstHrAlaAlaIatYrGlyHisphEgLYArGaSPaSPrOAS 377
210 CTTACCTGCGAGGTGTCAGAGCC 234
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377 pPheThrTrpGluValValIysPro 385
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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-51038
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; Sequence 51038, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51038
; LENGTH: 393
; TYPE: PRF
; ORGANISM: Brassica juncea
US-09-791-537-51038
```

```
alignment_scores:
  Quality: 120.00      Length: 25
  Ratio: 5.217        Gaps: 0
  Percent Similarity: 92.000      Percent Identity: 88.000
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alignment_block:
US-09-198-779B-1 x US-09-791-537-51038 ..
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Align seg 1/1 to: US-09-791-537-51038 from: 1 to: 393
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160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGAGCCGA 209
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361 ArgpheuLeuYstHrAlaAlaIatYrGlyHisphEgLYArGaSPaSPrOAS 377
210 CTTACCTGCGAGGTGTCAGAGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 pPheThrTrpGluValValIysPro 385
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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-85949
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seq_documentation_block:
; Sequence 85949, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M-
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85949
; LENGTH: 393
; TYPE: PRF
; ORGANISM: Lycopersicon esculentum
US-09-791-537-85949
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```
alignment_scores:
  Quality: 120.00      Length: 25
  Ratio: 5.217        Gaps: 0
  Percent Similarity: 92.000      Percent Identity: 88.000
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```
alignment_block:
US-09-198-779B-1 x US-09-791-537-85949 ..
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```
Align seg 1/1 to: US-09-791-537-85949 from: 1 to: 393
```

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361 ArgpheuLeuYstHrAlaAlaIatYrGlyHisphEgLYArGaSPaSPrOAS 377
210 CTTACCTGCGAGGTGTCAGAGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 pPheThrTrpGluValValIysPro 385
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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-85952
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seq_documentation_block:
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; Sequence 85952, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85952
; LENGTH: 393
; TYPE: PRF
; ORGANISM: Lycopersicon esculentum
US-09-791-537-85952
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alignment_scores:
  Quality: 120.00      Length: 25
  Ratio: 5.217        Gaps: 0
  Percent Similarity: 92.000      Percent Identity: 88.000
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```
alignment_block:
US-09-198-779B-1 x US-09-791-537-85952 ..
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```
Align seg 1/1 to: US-09-791-537-85952 from: 1 to: 393
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160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGAGCCGA 209
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Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

## alignment\_block:

US-09-198-779B-1 x US-09-791-537-124286 ..

Align seg 1/1 to: US-09-791-537-124286 from: 1 to: 394

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362 ArgpHeLeuYsThrAlaIaIaTyGlyHisPheGlyArgAspAspAlaAs 378  
210 CTTCACTCGCAGGTGTCAAGCCC 234  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
378 pPheHrTrpGluValIaIysPro 386

seq\_name: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-124294

## seq\_documentation\_block:

; Sequence 124294 Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 124294  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Actinidia chinensis  
US-09-791-537-124294

## alignment\_scores:

Quality: 125.00 Length: 25  
Ratio: 5.208 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 92.000

## alignment\_block:

US-09-198-779B-1 x US-09-791-537-124294 ..

Align seg 1/1 to: US-09-791-537-124294 from: 1 to: 360

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTGGCCGTGACGAGCGCGA 209  
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328 ArgpHeLeuYsThrAlaIaIaTyGlyHisPheGlyArgAspAspAlaAs 344  
210 CTTCACTCGCAGGTGTCAAGCCC 234  
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344 pPheHrTrpGluValIaIysPro 352

seq\_name: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-120896

## seq\_documentation\_block:

; Sequence 120896 Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 120896

; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Mesembryanthemum crystallinum  
US-09-791-537-120896

## alignment\_scores:

Quality: 122.00 Length: 25  
Ratio: 5.083 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 88.000

## alignment\_block:

US-09-198-779B-1 x US-09-791-537-120896 ..

Align seg 1/1 to: US-09-791-537-120896 from: 1 to: 392

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTGGCCGTGACGAGCGCGA 209  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
360 ArgTrLeuYsThrAlaIaIaTyGlyHisPheGlyArgAspAspAlaAs 376  
210 CTTCACTCGCAGGTGTCAAGCCC 234  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
376 pPheHrTrpGluValIaIysPro 384

seq\_name: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-122527

## seq\_documentation\_block:

; Sequence 122527 Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 122527  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Petunia x hybrida  
US-09-791-537-122527

## alignment\_scores:

Quality: 121.00 Length: 25  
Ratio: 5.042 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 88.000

## alignment\_block:

US-09-198-779B-1 x US-09-791-537-122527 ..

Align seg 1/1 to: US-09-791-537-122527 from: 1 to: 393

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTGGCCGTGACGAGCGCGA 209  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
361 ArgpHeLeuYsThrAlaIaIaTyGlyHisPheGlyArgAspAspThrAs 377  
210 CTTCACTCGCAGGTGTCAAGCCC 234  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
377 pPheHrTrpGluValIaIysPro 385

seq\_name: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:US-09-791-537-6453

## seq\_documentation\_block:

; Sequence 6453 Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph

OM of: US-09-198-779b-1 to: Pending\_Patents\_AA\_New:\* out\_format : pfs  
Date: Aug 20, 2002 2:52 AM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

## Command line parameters:

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-GAP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000  
-LOOPEXT=0.000 -OGAP=4.500 -OGAPEXT=0.050 -XGAP=10.000  
-XGAPEXT=0.500 -FGAP=6.000 -FGAPEXT=7.000 -YCAP=10.000  
-YCAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1  
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## Search information block:

Query: US-09-198-779b-1  
Query length: 235  
Database: Pending\_Patents\_AA\_New:\*  
Database sequences: 713468  
Database length: 23663020  
Search time (sec): 151.000000

## Score\_list:

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/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-124286			127.00	309.06	2.5e-09				
/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-124294			125.00	304.62	4.8e-09				
/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-120896			122.00	296.00	1.3e-08				
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/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-424-978b-36			117.00	282.81	7.2e-08				
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/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-124287			116.00	280.88	1.0e-07				
/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-424-978b-39			116.00	280.28	1.0e-07				
/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-120901			116.00	280.25	1.0e-07				
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/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-111335			101.00	241.00	1.6e-05				
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/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-84678			98.00	233.01	4.3e-05				
/cgcn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-136007			97.00	230.52	6.0e-05				
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seq\_name: /cgcn2\_6/ptodata/2/paa/US09\_NEW.COMB.pcp:US-09-424-978b-42

## seq\_documentation\_block:

Sequence 42, Application US/09424978B  
GENERAL INFORMATION:  
APPLICANT: Falco, Severio Carl  
APPLICANT: Allen, Stephen M.  
APPLICANT: Rafalski, J. Antoni  
APPLICANT: Hiltz, William D.  
APPLICANT: Kinney, Anthony J.  
APPLICANT: Abell, Lynne N.  
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
FILE REFERENCE: BB-1087  
CURRENT APPLICATION NUMBER: US/09/424,978B  
PRIOR APPLICATION NUMBER: 1999-12-02  
PRIOR FILING DATE: 1997-06-06  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 42  
LENGTH: 394  
TYPE: PRT  
ORGANISM: Triticum aestiva  
US-09-424-978b-42

alignment\_scores:  
Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

alignment\_block:  
US-09-198-779b-1 x US-09-424-978b-42 ..

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|||||  
362 ArgpHeIleIySThAlAlAtyrlYhSPheGIyAlGAsPAlAAs 378

210 CTTCACTGCGAGGTGTCAGCCC 234  
|||||

378 pPheHrTrIpGluValIyAlSPro 386

seq\_name: /cgcn2\_6/ptodata/2/paa/US09\_NEW.COMB.pcp:US-09-791-537-124286

## seq\_documentation\_block:

Sequence 124286, Application US/09791537  
GENERAL INFORMATION:  
APPLICANT: Biomox, Inc.  
APPLICANT: Debe, Derek  
APPLICANT: Danzer, Joseph  
TITLE OF INVENTION: METHODS OF USE THEREOF  
FILE REFERENCE: 261/210  
CURRENT APPLICATION NUMBER: US/09/791,537  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 124286  
LENGTH: 394  
TYPE: PRT  
ORGANISM: Hordeum vulgare  
US-09-791-537-124286

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|||||  
286 pphethrtprgluValValysPro 294

seq\_name: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep:US-09-708-427-50982

seq\_documentation\_block:

Sequence 50982, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50982

LENGTH: 339

TYPE: PRT

ORGANISM: Zea mays subsp. mays

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..339

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc\_feature

LOCATION: 1..339

OTHER INFORMATION: Ceres Seq. ID 1925818

US-09-708-427-50982

alignment\_scores:

Quality: 127.00 Length: 25

Ratio: 5.292 Gaps: 0

Percent Similarity: 96.000 Percent Identity: 96.000

alignment\_block:

US-09-198-779b-1 x US-09-708-427-50982 ..

Align seg 1/1 to: US-09-708-427-50982 from: 1 to: 339

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|||||

309 ArgpheiIeIySThrAlaIaIatYrGIhSPheGIyArGaSPaSPAlaAs 325

210 CTTCACTGCGAGGTGTCACGCC 234

|||||

325 pphethrtprgluValValysPro 333

seq\_name: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep:US-09-708-427-50981

seq\_documentation\_block:

Sequence 50981, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50981

LENGTH: 341

TYPE: PRT

ORGANISM: Zea mays subsp. mays

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..341

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc\_feature

LOCATION: 1..341

OTHER INFORMATION: Ceres Seq. ID 1925817

US-09-708-427-50981

alignment\_scores:

Quality: 127.00 Length: 25

Ratio: 5.292 Gaps: 0

Percent Similarity: 96.000 Percent Identity: 96.000

alignment\_block:

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Align seg 1/1 to: US-09-708-427-50981 from: 1 to: 341

160 AGGTCATCAAGACCGCGCATACGGCCACTTTGGCGGTGACGACGCCGA 209

|||||

311 ArgpheiIeIySThrAlaIaIatYrGIhSPheGIyArGaSPaSPAlaAs 327

210 CTTCACTGCGAGGTGTCACGCC 234

|||||

327 pphethrtprgluValValysPro 335

seq\_name: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:US-60-324-109-17286

seq\_documentation\_block:

Sequence 17286, Application US/60324109

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Edgerton, Michael D

APPLICANT: Hinkle, Gregory J.

APPLICANT: Kovalic, David K.

APPLICANT: Liu, Jindong

APPLICANT: Stein, Joshua

TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-10(52726)B

CURRENT APPLICATION NUMBER: US/60/324,109

CURRENT FILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 33196

SEQ ID NO 17286

LENGTH: 351

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

US-60-324-109-17286

alignment\_scores:

Quality: 127.00 Length: 25

Ratio: 5.292 Gaps: 0

Percent Similarity: 96.000 Percent Identity: 96.000

alignment\_block:

US-09-198-779b-1 x US-60-324-109-17286 ..

Align seg 1/1 to: US-60-324-109-17286 from: 1 to: 351

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|||||

319 ArgpheiIeIySThrAlaIaIatYrGIhSPheGIyArGaSPaSPAlaAs 335

210 CTTCACTGCGAGGTGTCACGCC 234

|||||

335 pphethrtprgluValValysPro 343

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; OTHER INFORMATION: Clone ID: 700430776_FLI
US-60-312-544-5922

alignment_scores:
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  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779b-1 x US-60-312-544-5922  ..

Align seg 1/1 to: US-60-312-544-5922 from: 1 to: 143

160 AGGTTTCATCAGACCGCCGATACGCGCCTTTGGCCGTGACGACGCCGA 209
|||||
111 ArgpHeIlelystHrAlaIaIatYrglyHIsPheGlyArgAspAspAlaAs 127
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
|||||
127 pPheHtrTpgIuValIySPro 135

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seq_documentation_block:
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; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 25804
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-25804

alignment_scores:
  Quality: 127.00      Length: 25
  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779b-1 x US-60-324-109-25804  ..

Align seg 1/1 to: US-60-324-109-25804 from: 1 to: 220

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|||||
188 ArgpHeIlelystHrAlaIaIatYrglyHIsPheGlyArgAspAspAlaAs 204
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
|||||
204 pPheHtrTpgIuValIySPro 212

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-26344

seq_documentation_block:
; Sequence 26344, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 6239
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-312-544-6239

OTHER INFORMATION: Clone ID: 700573489_FLI

alignment_scores:
  Quality: 127.00      Length: 25
  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779b-1 x US-60-312-544-6239  ..

Align seg 1/1 to: US-60-312-544-6239 from: 1 to: 302

160 AGGTTTCATCAGACCGCCGATACGCGCCTTTGGCCGTGACGACGCCGA 209
|||||
270 ArgpHeIlelystHrAlaIaIatYrglyHIsPheGlyArgAspAspAlaAs 286
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234

; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 26344
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-26344

alignment_scores:
  Quality: 127.00      Length: 25
  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779b-1 x US-60-324-109-26344  ..

Align seg 1/1 to: US-60-324-109-26344 from: 1 to: 262

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|||||
230 ArgpHeIlelystHrAlaIaIatYrglyHIsPheGlyArgAspAspAlaAs 246
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
|||||
246 pPheHtrTpgIuValIySPro 254

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-312-544-6239

seq_documentation_block:
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; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 6239
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-312-544-6239

OTHER INFORMATION: Clone ID: 700573489_FLI

alignment_scores:
  Quality: 127.00      Length: 25
  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
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Align seg 1/1 to: US-60-312-544-6239 from: 1 to: 302

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270 ArgpHeIlelystHrAlaIaIatYrglyHIsPheGlyArgAspAspAlaAs 286
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
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; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 28766
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-28766

alignment_scores:
Quality: 127.00      Length: 25
Ratio: 5.292        Gaps: 0
Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-324-109-28766 ..

Align seg 1/1 to: US-60-324-109-28766 from: 1 to: 116

160 AGGTCATCATAGAGCCGCGCATATAGCGCACTTGGCCGTGAGAGAGCCGA 209
|||||
84 ArgpheiIeIysthAlaIaIaIyrgIyHspneGIyArgAspAspAlaAs 100
210 CTTCACCTGCGAGGTGTCAGCC 234
|||||
100 pPheHtrTpGluValIaIyIysPro 108

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pap:US-60-324-109-26158

seq_documentation_block:
; Sequence 26158, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 26158
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-26158

alignment_scores:
Quality: 127.00      Length: 25
Ratio: 5.292        Gaps: 0
Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-324-109-26158 ..

Align seg 1/1 to: US-60-324-109-26158 from: 1 to: 132

160 AGGTCATCATAGAGCCGCGCATATAGCGCACTTGGCCGTGAGAGAGCCGA 209
|||||
106 ArgpheiIeIysthAlaIaIaIyrgIyHspneGIyArgAspAspAlaAs 122
210 CTTCACCTGCGAGGTGTCAGCC 234
|||||
122 pPheHtrTpGluValIaIyIysPro 130

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pap:US-60-312-544-5922

seq_documentation_block:
; Sequence 5922, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 5922
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-312-544-8313

seq_documentation_block:
; Sequence 8313, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 8313
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-312-544-8313

alignment_scores:
Quality: 127.00      Length: 25
Ratio: 5.292        Gaps: 0
Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-312-544-8313 ..

Align seg 1/1 to: US-60-312-544-8313 from: 1 to: 138

160 AGGTCATCATAGAGCCGCGCATATAGCGCACTTGGCCGTGAGAGAGCCGA 209
|||||
106 ArgpheiIeIysthAlaIaIaIyrgIyHspneGIyArgAspAspAlaAs 122
210 CTTCACCTGCGAGGTGTCAGCC 234
|||||
122 pPheHtrTpGluValIaIyIysPro 130
```



## alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

## alignment\_block:

US-09-198-779b-1 x US-60-324-109-31671 ..

Align seg 1/1 to: US-60-324-109-31671 from: 1 to: 79

```

160 AGGTCATCATAGACCGCCGATACGGCAGCTTTGGCCGTGAGACGCGCA 209
|||||
47 ArgpheiellisthrAlaIatYrgIyHisphegIyArGAspAspAlaAs 63
|||||
210 CTTCACTGCGAGGTGTCAGCCC 234
|||||
63 pPheHrTrpGIuValIyAllysPro 71

```

seq\_name: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:US-60-324-109-18261

## seq\_documentation\_block:

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: Sequence 18261, Application US/60324109
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Edgerton, Michael D
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Kovallie, David K.
: APPLICANT: Liu, Jindong
: APPLICANT: Stein, Joshua
: TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
: FILE REFERENCE: 38-10(52726)B
: CURRENT APPLICATION NUMBER: US/60/324,109
: NUMBER OF FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 33196
: SEQ ID NO 18261
: LENGTH: 82
: TYPE: PRT
: ORGANISM: Zea mays
: FEATURE:
: US-60-324-109-18261

```

## alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

## alignment\_block:

US-09-198-779b-1 x US-60-324-109-18261 ..

Align seg 1/1 to: US-60-324-109-18261 from: 1 to: 82

```

160 AGGTCATCATAGACCGCCGATACGGCAGCTTTGGCCGTGAGACGCGCA 209
|||||
52 ArgpheiellisthrAlaIatYrgIyHisphegIyArGAspAspAlaAs 68
|||||
210 CTTCACTGCGAGGTGTCAGCCC 234
|||||
68 pPheHrTrpGIuValIyAllysPro 76

```

seq\_name: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:US-60-324-109-27080

## seq\_documentation\_block:

```

: Sequence 27080, Application US/60324109
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Edgerton, Michael D
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Kovallie, David K.
: APPLICANT: Liu, Jindong
: APPLICANT: Stein, Joshua
: TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
: FILE REFERENCE: 38-10(52726)B

```

: CURRENT APPLICATION NUMBER: US/60/324,109

: CURRENT FILING DATE: 2001-09-21

: NUMBER OF SEQ ID NOS: 33196

: SEQ ID NO 27080

: LENGTH: 90

: TYPE: PRT

: ORGANISM: Zea mays subsp. mexicana

: FEATURE:

## alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

## alignment\_block:

US-09-198-779b-1 x US-60-324-109-27080 ..

Align seg 1/1 to: US-60-324-109-27080 from: 1 to: 90

```

160 AGGTCATCATAGACCGCCGATACGGCAGCTTTGGCCGTGAGACGCGCA 209
|||||
58 ArgpheiellisthrAlaIatYrgIyHisphegIyArGAspAspAlaAs 74
|||||
210 CTTCACTGCGAGGTGTCAGCCC 234
|||||
74 pPheHrTrpGIuValIyAllysPro 82

```

seq\_name: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:US-60-324-109-17432

## seq\_documentation\_block:

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: Sequence 17432, Application US/60324109
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Edgerton, Michael D
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Kovallie, David K.
: APPLICANT: Liu, Jindong
: APPLICANT: Stein, Joshua
: TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
: FILE REFERENCE: 38-10(52726)B
: CURRENT APPLICATION NUMBER: US/60/324,109
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 33196
: SEQ ID NO 17432
: LENGTH: 92
: TYPE: PRT
: ORGANISM: Zea mays
: FEATURE:
: US-60-324-109-17432

```

## alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

## alignment\_block:

US-09-198-779b-1 x US-60-324-109-17432 ..

Align seg 1/1 to: US-60-324-109-17432 from: 1 to: 92

```

160 AGGTCATCATAGACCGCCGATACGGCAGCTTTGGCCGTGAGACGCGCA 209
|||||
60 ArgpheiellisthrAlaIatYrgIyHisphegIyArGAspAspAlaAs 76
|||||
210 CTTCACTGCGAGGTGTCAGCCC 234
|||||
76 pPheHrTrpGIuValIyAllysPro 84

```

seq\_name: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:US-60-324-109-28766

OM of: US-09-198-779b-1 to: Pending\_Patents\_AA\_Main.\* out\_format : pfs  
Date: Aug 20, 2002 2:49 AM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

## Command line parameters:

-MODEL=framed\_n2p.model -DEV=xlp  
-O=/cg2\_1/USPRO.spool/US09198779/runtat\_19082002\_140849\_23728/app\_query.fasta\_1.296  
-DB=Pending\_Patents\_AA\_Main -QMT=fastan -SUFFIX=rapm  
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000  
-LOOPEXT=0.000 -OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000  
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000  
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1  
-MATRIX=biosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200  
-THR\_SCORE=pcet -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pts -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USBR=US09198779.@CGNL\_1\_231 -NCPU=6 -ICPU=3 -LONGIOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPHY -WAIT -THREADS=1

## Search information block:

Query: US-09-198-779b-1  
Query length: 235  
Database: Pending\_Patents\_AA\_Main.\*  
Database sequences: 3502263  
Database length: 351980561  
Search time (sec): 316.510000

## score\_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation	..
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-312-544-9603			127.00	327.36	2.9e-09	48
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-18671			127.00	323.28	3.0e-09	79
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-18261			127.00	322.97	3.0e-09	82
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-27080			127.00	322.21	3.0e-09	90
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17432			127.00	322.03	3.0e-09	92
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-28766			127.00	320.13	3.0e-09	116
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-312-544-8313			127.00	319.07	3.1e-09	132
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-312-544-5922			127.00	318.71	3.1e-09	138
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-25804			127.00	314.88	3.1e-09	143
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-26344			127.00	313.45	3.2e-09	220
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-312-544-6239			127.00	312.29	3.2e-09	262
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-108-427-50982			127.00	311.34	3.2e-09	302
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-108-427-50981			127.00	311.29	3.2e-09	33
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17286			127.00	311.05	3.2e-09	34
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-19530			127.00	310.94	3.2e-09	351
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-108-427-50980			127.00	310.15	3.2e-09	356
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17569			127.00	310.15	3.2e-09	392
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17652			127.00	310.15	3.2e-09	392
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-19482			127.00	310.15	3.2e-09	392
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-28912			127.00	310.15	3.2e-09	392
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-29461			127.00	310.15	3.2e-09	392
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17609			127.00	310.11	3.2e-09	394
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-19033			127.00	310.11	3.2e-09	394
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-28758			127.00	310.11	3.2e-09	394
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17623			127.00	309.88	3.2e-09	405
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-620-394B-944			125.00	312.77	6.1e-09	148
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-620-394B-943			125.00	312.77	6.1e-09	150
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-620-394B-942			125.00	311.79	6.4e-09	165
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-11464			125.00	304.85	6.4e-09	394
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-31541			125.00	304.85	6.4e-09	394
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-325-849-6			121.00	309.23	2.2e-08	64
/cg2_6/ptodata/2/paa/US093.COMB.pep:US-09-595-329A-2052			120.00	299.84	3.4e-08	34
/cg2_6/ptodata/2/paa/US095.COMB.pep:US-09-595-329A-2051			120.00	299.84	3.4e-08	34
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-20985			120.00	292.18	3.4e-08	372
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-09-595-329A-2050			120.00	291.71	3.4e-08	372
/cg2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-19977			120.00	291.71	3.4e-08	394

/cg2\_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-21800 + 120.00 291.71 3.4e-08  
/cg2\_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-22927 + 120.00 291.71 3.4e-08  
/cg2\_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-23049 + 120.00 291.71 3.4e-08  
/cg2\_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-23205 + 120.00 291.71 3.4e-08  
/cg2\_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-23229 + 120.00 291.71 3.4e-08

seq\_name: /cg2\_6/ptodata/2/paa/US60.COMB.pep:US-60-312-544-9603

## seq\_documentation\_block:

Sequence 9603, Application US/60312544  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Edgerton, Michael D  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jindong  
APPLICANT: Stein, Joshua  
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-10(52726)A  
CURRENT APPLICATION NUMBER: US/60/312,544  
CURRENT FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 10730  
SEQ ID NO 9603  
LENGTH: 48  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3205-165-H12\_FLI  
US-60-312-544-9603

## alignment\_scores:

Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000

## alignment\_block:

US-09-198-779b-1 x US-60-312-544-9603 ..  
Align seg 1/1 to: US-60-312-544-9603 from: 1 to: 48

160 AGCTTCATCAGACCGCCGATAGCGCCACTTGGCCGTGACGACCGCA 209  
|||||  
16 ATGpHeiIeIyThrAlaAlaIyrcIyHegIyATGAspAspAlaAs 32

210 CTTGACCGCGAGCGGTCACGCC 234  
|||||

32 pHeItrIrpGluValValysPro 40

seq\_name: /cg2\_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-31671

## seq\_documentation\_block:

Sequence 31671, Application US/60324109  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Edgerton, Michael D  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jindong  
APPLICANT: Stein, Joshua  
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-10(52726)B  
CURRENT APPLICATION NUMBER: US/60/324,109  
CURRENT FILING DATE: 2001-09-21  
NUMBER OF SEQ ID NOS: 33196  
SEQ ID NO 31671  
LENGTH: 79  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
US-60-324-109-31671

FEATURES	FT	source	1. .1182
source	FT	Location/Qualifiers	/organism='Hordeum vulgare'.
		1. .1182	
BASE COUNT		253 a	368 c 331 g 230 t
ORIGIN			
Query Match	Best Local Similarity	26.2%;	Score 61.6; DB 6; Length 1182;
Matches	67; Conservative	0; Mismatches	9; Indels 0; Gaps 0;
OY	159	caggttcataaagccgcgcacatagccgaccttggccgtagacgacgaccttaacctg	218
Db	1083	CAGGTTCAATCAAGACAGACTGCTTACGGTCACTTTGGCCGCGATGATGCTGACTTCACTCG	1143
OY	219	cgaagtggtgtaagcccc	235
Db	1143	GGAGTGGTGAAGCCCC	1159
RESULT	4		
LOCUS	E14402	1182 bp	DNA linear PAT 28-JUL-1999
DEFINITION	cDNA encoding S-adenosylmethionine synthetase.		
ACCESSION	E14402		
VERSION	E14402.1 GI:5709085		
KEYWORDS	JP 1997313186-A/1.		
SOURCE	Hordeum vulgare.		
ORGANISM	Hordeum vulgare		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	Poideae; Triticeae; Hordeum.		
	1 (bases 1 to 1182)		
REFERENCE	MORI,S.		
AUTHORS	GENE OF S-ADENOSYLMETHIONINE SYNTHASE		
TITLE	Patent: JP 1997313186-A 1 09-DEC-1997;		
JOURNAL	NIPPON OIL CO LTD		
COMMENT	OS Hordeum vulgare		
	PN JP 1997313186-A/1		
	PD 09-DEC-1997		
	PF 28-MAY-1996 JP 1996133406		
	PI MORI SATOSHI		
	PC C12N15/09,C07H21/04,C12N9/00//A01H1/00,A01H5/00; CC		
	strandedness: Double;		
	CC topology: Linear;		
	CC hypothetical: No;		
	CC anti-sense: No;		
	FT	Key	Location/Qualifiers
	FT	source	1. .1182
	FT		Location/Qualifiers
FEATURES	source	Location/Qualifiers	/organism='Hordeum vulgare'.
		1. .1182	
		/organism='Hordeum vulgare'	
		/db_xref='taxon:4513'	
BASE COUNT	253 a	372 c	324 g 233 t
ORIGIN			
Query Match	Best Local Similarity	26.0%;	Score 61; DB 6; Length 1182;
Matches	67; Conservative	0; Mismatches	10; Indels 0; Gaps 0;
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Db	1083	CAGGTTCAATCAAGACAGACTGCTTACGGTCACTTTGGCCGCGATGATGCTGACTTCACTCG	1143
OY	219	cgaagtggtgtaagcccc	235
Db	1143	GGAGTGGTGAAGCCCC	1159

[illegible]

	REFERENCE	1 (bases 1 to 1182)
AUTHORS	Mori,S.	
TITLE	GENE OF S-ADENOSYL METHIONINE SYNTHASE	
JOURNAL	Patent: JP 1997313186-A 2 09-DEC-1997; NIPPON OIL CO LTD OS	
COMMENT	Hordeum vulgare PN JP 1997313186-A/2 PD 09-DEC-1997 PF 28-MAY-1996 JP 1996133406 PI MORI SATOSHI PC C12M15/09,C07H21/04,C12N9/00//A01H1/00,A01H5/00; CC strandedness: Double;	
	CC topology: linear;	
	CC hypothetical: No;	
	CC anti-sense: No;	
FH	Key	Location/Qualifiers
FT	source	1..1182
FEATURES	/db_xref=taxon:4513"	'organism='Hordeum vulgare'.
SOURCE	location/Qualifiers	
	1..1182	
BASE COUNT	261 a 368 c 324 g 229 t	
ORIGIN		
Query Match	25.3%; Score 59.4; DB 6; Length 1182;	
Best Local Similarity	85.7%; Pred. No. 4.7e-07;	
Matches	66; Conservative 0; Mismatches 11; Indels 0; Gaps 0,	
OY	159 caggttcatacaaggccgcacatcggcgactttgccgctgaacgcgcgatattaccctg 218	
Dd	tcccc	
	CAGGTTCAATCAGAACAACGTCTTACC GTACTTCGGCGCATGCTGCATTCACTGCC 1142	
OY	219 cgaaagtgtccaagccc 235	
Dd	t	
	GGAAGTGCTGAAGCCCC 1159	
RESULT	7 .	
AF420238 LOCUS	1566 bp mRNA Linear PLN 18-OCT-2001	
DEFINITION	Dendrobium crumenatum s-adenosyl-L-methionine synthetase (Sams)	
ACCESSION	mRNA, complete cds.	
VERSION	AF420238	
KEYWORDS	AF420238.1 GI:16226058	
SOURCE ORGANISM	.	
	Dendrobium crumenatum.	
	Dendrobium crumenatum	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;	
	Epidendroideae; higher Epidendroideae; Dendroleae; Dendrobiinae;	
	Dendrobium.	
	1 (bases 1 to 1566)	
REFERENCE AUTHORS TITLE JOURNAL	Han,P. and Pua,E.C. Direct Submission Submitted (17-SEP-2001) Department of Biological Sciences, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260	
FEATURES	Location/Qualifiers	
source	1..1566	
	/organism="Dendrobium crumenatum"	
	/db_xref="taxon:51096"	
	1..1566	
gene	/gene="Sams"	
	74..1261	
CDS	/gene="Sams"	
	/codon_start=1	
	/product="-S'-adenosyl-L-methionine synthetase"	
	/protein_id="AA116064.1"	
	/db_xref="GI:16226059"	
	/translation="MAEVDFLFSTSVNGHDKLCDDQISDLIDACLKEQDPDSKYA CEFCGSTNMVIMIGETITTKANDVIYEKVDTFCAIGVSDDVGILDNCNVLVNIIEQQ	

BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	64; Conservative	23.9%; Score 56.2; DB 8; Length 1566; Pred. No. 4.3e-06; Mismatches 13; Indels 0; Gaps 0;
385 a	393 c	411 g	377 t			
QY	159	caggttcacaaagaccgcccgcataagccactttgcccgtgacgacgcgcagcttacctg	218			
Db	1159	CCGGTTCATCAAGACGGCGGGCTACGGCCACTTGGAGAGATGACCCCTGATTTCACCTG	1218			
QY	219	cgaggtgtcaagcccc	235			
Db	1219	GGAGGTGTGTAAGCCCC	1235			
RESULT	8	OSU82833	1736 bp	mrna	linear	PLN 12-MAR-1998
LOCUS		OSU82833				
DEFINITION		Oryza sativa S-adenosyl-L-methionine synthetase (pos-SAMS2) mRNA,				
ACCESSION		complete cds.				
VERSION		082833				
KEYWORDS		082833.1 GI:1778820				
SOURCE		Oryza sativa.				
ORGANISM		Oryza sativa.				
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
AUTHORS		1 (bases 1 to 1736)				
		Lee,J.H., Chae,H.S., Lee,J.H., Hwang,B., Hahn,K.W., Kang,B.G. and Kim,W.T.				
TITLE		Structure and expression of two cDNAs encoding S-adenosyl-L-methionine synthetase of rice (Oryza sativa L.)				
JOURNAL		Biochim. Biophys. Acta 1354 (1), 13-18 (1997)				
MEDLINE		98041632				
REFERENCE		2 (bases 1 to 1736)				
AUTHORS		Kim,W.T.				
TITLE		Direct Submission				
JOURNAL		Submitted (20-DEC-1996) Biology, Yonsei University, Shinchon-dong 134, Seodaemun-gu, Seoul 120-749, South Korea				
FEATURES		Location/Qualifiers				
source		1..1736				
gene		/organism="Oryza sativa"				
		/db_xref="taxon:4530"				
		1..1736				
		/gene="pos-SAMS2"				
		127..1311				
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		/codon_start=1				
		/product="S-adenosyl-L-methionine synthetase"				
		/protein_id="AAC05590.1"				
		/db_xref="GI:1778821"				
		/translation="MAEPTLFSTSEVNEGHPDKLDQVSDAVLDACIADPPSKYAC ECTCTRMVAVFGEITTKATVDTEKIVRDCRIGFVSDVGIDARCKVLYVNI EDS PDLAQVGHGHTKRPEIGAGDGHMFVATDTPELMPLSHYLATRLGARLKEVKN GTGAMLRPDGKTQVTVLEYLNDAGAMPVRVHTVLTSTOHDEVTNDEIAADLKEHYK PVPIDKLEKDTLFHLNPSGRFVIGGPHGAGLTGRKTIIDTGGGARGGGAGFSGKD PTVDSGAYIARQAAKSIYASGLARICVQVYATGCPREPISVPVDSYCTGKIPKE IKTIVENEDPFRGMMTINLDLKRGGNRLFKTAAYGHGREDDPTWEVYKPLKTEKA SS"				
CDS						
BASE COUNT	370 a	563 c	481 g	322 t		
ORIGIN						







<b>LOCUS</b>	DINCARAA	1632 bp	mRNA	linear	PIN 03-MAR-1994
<b>DEFINITION</b>	D.caryophyllus S-adenosylmethionine synthetase (CARSAM2) mRNA, complete cds.				
<b>ACCESSION</b>	M61882				
<b>KEYWORDS</b>	G1:167961				
<b>SOURCE</b>	S-adenosylmethionine synthetase. D.caryophyllus petal, cDNA to mRNA, clone pSAM2. Dianthus caryophyllus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Dianthus. 1 (bases 1 to 1632)				
<b>REFERENCE</b>	Larsen,P.B. and Woodson,W.R. Cloning and nucleotide sequence of a s'-adenosylmethionine synthetase cDNA clone from carnation Plant Physiol. (1991) In press				
<b>AUTHORS</b>	Location/Qualifiers 1..1632				
<b>TITLE</b>	/organism="Dianthus caryophyllus" /db_xref="taxon:3570"				
<b>JOURNAL</b>	1..1632				
<b>FEATURES</b>	/gene="CARSAM2" 72..1262 /gene="CARSAM2" /codon_start=1 /product="S-adenosylmethionine synthetase" /protein_id="AAA33274.1" /db_xref="GI:304637" /translation="MAAADPFLTFSVNEGHPDKIDISDAVIDACLQAQAESEV ACEFCKTNLVMGGEITTKRANDEYKIVADTCETGFSPVDGLDNCKVLVIHQ OSPDIAAGVCHLTRPEDDVGGMFGVADTEPELPSHLATKIGARTVEVR KNGICAMLRPDGKTQVTVEYNENGAQMPRLRHVTLISTHEDERVNDETAADLKEHV IKPVIPERYIDENTIFHLINSGREVIGAGVDAGLTGRKLIIDRYGGMGAHGGAFFSR KDPLKRVDSGAVIAROAKSIVSGIARRCIVOISVIGPEPLSVFDVPGTGKTHD RELIKVIKENDFPRGMIALIALDLCKGNLYLRTAAIGHRGREDPTWEAKTLKME KPQA"				
<b>BASE COUNT</b>	405 a	383 c	424 g	420 t	
<b>ORIGIN</b>					
Query Match	21.8%	Score 51.2;	DB 8;	Length 1632;	
Best Local Similarity	53.0%;	Pred. No. 0.00013;			
Matches 62:	Conservative	0;	Mismatches 55;	Indels 0;	Gaps 0;
<b>QY</b>	119	gtlnnccaggttcatacaagccgcg 178			
<b>Db</b>	1120	GTATGATGCAGCCATTGCCCTCGACTCAAGAAGGTTGGGACACAGGTACTTGAAGCACAGCCG 1179			
<b>QY</b>	179	catcggccactcttgccgcyaacgacgcgcgaattcacctcgagagtgtgaagcccc 235			
<b>Db</b>	1180	CGTAGTGACACTTGTGACAGTGGAAGACCCTCGACTCAGCTGGAGAGCGTCAAGAAGCCC 1236			
<b>RESULT 17</b>					
<b>LOCUS</b>	OSA296743	1594 bp	mRNA	linear	PLN 10-DEC-2001
<b>DEFINITION</b>	Oryza sativa mRNA for s'-adenosylmethionine synthetase (SAMS gene).				
<b>ACCESSION</b>	AJ296743				
<b>VERSION</b>	AJ296743.1	G1:17529620			
<b>KEYWORDS</b>	S-adenosylmethionine synthetase; SAMS gene.				
<b>SOURCE</b>	Oryza sativa.				
<b>ORGANISM</b>	Oryza sativa				
<b>REFERENCE</b>	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
<b>AUTHORS</b>	Ehrhartoidese; Oryzae; Oryza.				
<b>TITLE</b>	1 (sites)				
<b>JOURNAL</b>	Mukhopadhyay,A., Sharma,S. and Tyagi,A.K.				
<b>REFERENCE</b>	Isolation and characterization of a new member of the rice S-adenosyl-L-methionine synthetase family				
<b>AUTHORS</b>	Unpublished				
<b>TITLE</b>	2 (bases 1 to 1594)				
<b>Direct Submission</b>	Tyagi,A.K.				

JOURNAL	Submitted (21-AUG-2000) Tyagi A.K., Department of Plant Molecular Biology, University of Delhi South Campus, Benito Juarez Road, New-Delhi, INDIA			
FEATURES	Location/Qualifiers			
Source	1. .1594			
	/organism="Oryza sativa"			
	/variety="Pusa Basmati 1"			
	/db_xref="taxon:4530"			
	/tissue_11b="Root"			
gene	108. .1298			
	/gene="SAMS"			
CDS	108. .1298			
	/gene="SAMS"			
	/EC_number="2.5.1.6"			
	/codon_start=1			
	/product="S-adenosylmethionine synthetase"			
	/protein_id="CAC82203.1"			
	/db_xref="GI:17529621"			
	/translation="MAADLTFLTSESNEGHPDKLDOVSDAVIDACLAEDPSKYAA CECTKTNMVMVFGELITTKAVDYEKIVRETCRNIGFVSADVGADADHCYKLVNI EDO SPDIAOGVHGHTKRPBEIIGAGDGHMGVATDTEPELMPLSHVLATKARLKVKK NGTCAMLRPDGKTQVTVYRNESGARVPVHVLISIOHDETVINDEIADLKEHVI KPTVEOYLDEKTEIFHLNPSGRFVYGPHGDAGLGRKLIIDTVGGMGAGGGAFFSKK LDVTRSGAVAVARQAASIVASGLARCIYQVSXAIQVPEPLSPVDYTGCTGAIIPK ELIKVKNPDPFRMTIINIDLKKGNGRILKTAIGHREDDPDTWEYVKPLKWE KPSA"			
BASE COUNT	374 a	433 c	406 g	381 t
ORIGIN				
Query Match	21.7%; Score 51; DB 8; Length 1594;			
Best Local Similarity	80.0%; Pred. No. 0.00015;			
Matches	60; Conservative	0; Mismatches	15; Indels	0; Gaps
OY	161	gggtcatcaagccgcgcacatagcgcacattgacgcgtgacagcgacgacttcacctgcg	220	
Db	1198	gctactctcaagcggcgcttaccgcttaccgacggaagcagaccagacttaccctggc	1257	
OY	221	agggtgltcaagcccc	235	
Db	1258	aggtgtgtaagcccc	1272	
RESULT	18			
LOCUS	OSSAMS1			
DEFINITION	2183 bp DNA linear PLN 06-DEC-1994			
ACCESSION	O.sativa (PFSAM-1) gene for S-adenosyl methionine synthetase.			
VERSION	226867.1 GI:450548			
KEYWORDS	S-adenosylmethionine synthetase.			
SOURCE	Oryza sativa.			
ORGANISM	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehretidoideae; Oryzaceae; Oryza.			
REFERENCE	1 (bases 1 to 2182)			
AUTHORS	Van Breusegem,F., Dekeyser,R., Gielens,J., Van Montagu,M. and Caplan,A.			
TITLE	Characterization of a S-adenosylmethionine synthetase gene in rice			
JOURNLM	Plant Physiol. 105 (4), 1463-1464 (1994)			
MEDLINE	95062735			
REFERENCE	2 (bases 1 to 2183)			
AUTHORS	Van Breusegem,F.			
TITLE	Direct Submission			
JOURNLM	Submitted (08-OCT-1993) Van Breusegem F., Universiteit Gent, Labo voor Genetika, Ledeganckstraat 35, Gent, Belgium, 9000			
REMARK	revised by [3] MAT			
REFERENCE	3 (bases 1 to 2183)			
AUTHORS	Van Breusegem,F.			
TITLE	Direct Submission			
JOURNLM	Submitted (25-JAN-1994) Van Breusegem F., Universiteit Gent, Labo voor Genetika, Ledeganckstraat 35, Gent, Belgium, 9000			
COMMENT	On Jan 26, 1994 this sequence version replaced gi:407153.			



[illegible]

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Kim, C.J., Chen, H., Cheuk, R., Koesema, E., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinzaki, K., Theologis, A., and Ecker, J.R.

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

## FEATURES

## SOURCE

Location/Qualifiers

1..1107

/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/chromosome="1"

/clone="U13694"

/note="This clone is in pU1 51"

ecotype: Columbia"

## CDS

1..1107

/note="s-adenosylmethionine synthetase"

/codon\_start=1

/product="At1g02500/714P4\_22"

/protein\_id="FAL31222.1"

/db\_xref="GI:16974437"

/translation="MOSSMPALNKTITAKILVRHAPPTMSNLSVRSPLLTTRRLSVTPVAFVSDVDGADKCKVYNTEQSPDIAQVHGHTFCPEITGGDGHMFIRHFTVLISTQHDTEVTNDEIARLKEHVAKPVEKYLDEKTIFFHNPGRFVIGPBGDGLGRKIIIDTYGWMGAHGGAGSPKPTVRSAGAVIVQAKSVANMARALVQVSAIGVPEPLSVFVDETGLIPDEKILIKVESFDFRGMNTINDLRGNGRFLKTAAYGHFGSDDDPFTWEYVKKPLKMDKPOA"

## BASE COUNT

307 a 278 c 278 g 244 t

## ORIGIN

## Query Match

Best Local Similarity 21.4%; Score 50.4; DB 8; Length 1107; Pred. No. 0.00022;

## Matches

60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

## QY

160 aggttcataagacgcgcgcacattggcgcgtgacgcgcgcacattcactgc 219

## Db

1006 AGGTTCTTGAAGAACTGGCGCTTACGACACTTGGAGAGACACCTGACTTACCTGG 1065

## QY

220 gaagtgatcaagcccc 235

## Db

1066 GAAGTCGTCAAGCCAC 1081

## RESULT 21

## AF428440

1440 bp mRNA linear PLN 18-OCT-2001

## LOCUS

Arabidopsis thaliana At1g02500/714P4\_22 mRNA, complete cds.

## DEFINITION

AF428440.1 GI:16226594

## ACCESSION

AF428440.1

## VERSION

1.1

## KEYWORDS

FLI cDNA.

## SOURCE

Arabidopsis thaliana

## ORGANISM

Arabidopsis thaliana

## REFERENCE

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Eudicotyledons: core eudicots: Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis. 1 (bases 1 to 1440)

## AUTHORS

Chen, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinzaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.

## TITLE

Arabidopsis cDNA clones

## JOURNAL

unpublished

## REFERENCE

## AUTHORS

2 (bases 1 to 1440)

## TITLE

## JOURNAL

Chen, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinzaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.

## COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinzaki, K.

## COMMENT

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

## COMMENT

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

## COMMENT

Location/Qualifiers

## COMMENT

1..1440

## COMMENT

/organism="Arabidopsis thaliana"

## COMMENT

/db\_xref="taxon:3702"

## COMMENT

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1..126

## COMMENT

127..1308

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/note="s-adenosylmethionine synthetase"

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## COMMENT

/db\_xref="GI:16226595"

## COMMENT

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## COMMENT

1309..1440

## COMMENT

3' UTR

## COMMENT

BASE COUNT

## COMMENT

381 a 353 c 334 g 372 t

## COMMENT

ORIGIN

## COMMENT

Query Match

## COMMENT

Best Local Similarity 21.4%; Score 50.4; DB 8; Length 1440; Pred. No. 0.00023;

## COMMENT

Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

## COMMENT

QY 160 aggttcataagacgcgcgcacattggcgcgtgacgcgcgcacattcactgc 219

## COMMENT

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## COMMENT

QY 220 gaagtgatcaagcccc 235

## COMMENT

Db 1267 GAAGTCGTCAAGCCAC 1282

## COMMENT

RESULT 22

AY052311 1459 bp mRNA linear PLN 05-SEP-2001  
 LOCUS Arabidopsis thaliana At1g02500/T14P4\_22 mRNA, complete cds.  
 DEFINITION AY052311  
 ACCESSION AY052311.1 GI:15450420  
 VERSION FLI\_CDNA.  
 KEYWORDS  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
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 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
 Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;  
 Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 1459)  
 REFERENCE  
 AUTHORS Shin,P., Chen,H., Cheuk,R., Kim,C.J., Koeseema,E., Meyers,M.C.,  
 Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D.,  
 Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A.,  
 Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,  
 Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J.,  
 Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A.,  
 Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,  
 Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.  
 Arabidopsis cDNA clones  
 Unpublished  
 2 (bases 1 to 1459)  
 TITLE  
 JOURNAL Submitted (17-AUG-2001) Salk Institute Genomic Analysis Laboratory  
 (SIGAL), Plant Biology Laboratory, The Salk Institute for  
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
 USA  
 COMMENT  
 RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
 Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.  
 The Salk, Stanford, PGEC (SSP) Consortium members carried out the  
 sequencing and annotation of the RAFL cDNAs: Shin,P., Chen,H.,  
 Cheuk,R., Kim,C.J., Koeseema,E., Meyers,M.C., Banh,J., Bowser,L.,  
 Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,  
 Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,  
 Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,  
 Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,  
 Davis,R.W., Theologis,A. and Ecker,J.R.  
 Shin,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to  
 this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)  
 contributed equally to this work as PIs.  
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 IHWVYVLSTQIDETVNDIARDLKEHVIKPKYIDETKIFLNLNSGRVIGGP  
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 Best local similarity 78.9%; Pred. No. 0.00023;  
 Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
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 ORGANISM Arabidopsis thaliana  
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 Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;  
 Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 1508)  
 REFERENCE  
 AUTHORS Shin,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C.,  
 Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D.,  
 Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,  
 Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H.,  
 Southwick,A., Toriumi,M., Yamada,K., Yu,G., Davis,R.W.,  
 Theologis,A. and Ecker,J.R.  
 Arabidopsis cDNA clones  
 Unpublished  
 2 (bases 1 to 1508)  
 TITLE  
 JOURNAL Submitted (30-NOV-2000) Salk Institute Genomic Analysis Laboratory  
 (SIGAL), Plant Biology Laboratory, The Salk Institute for  
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
 USA  
 COMMENT  
 RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
 Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.  
 On Mar 16, 2001 this sequence version replaced gi:11762285.  
 RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
 Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.  
 Shin,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C.,  
 Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D.,  
 Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,  
 Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H.,  
 Southwick,A., Toriumi,M., Yamada,K., Yu,G., Davis,R.W.,  
 Theologis,A. and Ecker,J.R.  
 Submitted (16-MAR-2001) Salk Institute Genomic Analysis Laboratory  
 (SIGAL), Plant Biology Laboratory, The Salk Institute for  
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
 USA

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Tracy, S.E., Banh, J., Bowser, L., Chung, M.K., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

## FEATURES

Location/Qualifiers

1..1508

/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/chromosome="1"

/clone="002C07E12(578)"

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## ORIGIN

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Tracy, S.E., Banh, J., Bowser, L., Chung, M.K., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

## FEATURES

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Location/Qualifiers

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/chromosome="3"

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1269..1510

BASE COUNT 400 a 310 c 361 g 439 t

## ORIGIN

## Query Match

Best Local Similarity 21.4%; Score 50.4; DB 8; Length 1510;

Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

## REFERENCE

1 (bases 1 to 1510)  
Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Tracy, S.E., Banh, J., Bowser, L., Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,

Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.

## REFERENCE

AUTHORS

Unpublished

2 (bases 1 to 1510)

Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Tracy, S.E., Banh, J., Bowser, L., Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.

Direct Submission

Submitted (22-MAY-2001) Salk Institute Genomic Analysis Laboratory (Stigall), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

## COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

## TITLE

JOURNAL

Unpublished

2 (bases 1 to 1510)

Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Tracy, S.E., Banh, J., Bowser, L., Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.

Direct Submission

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Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers

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/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/chromosome="3"

/clone="RAFL02-08-J05(R12690)"

/note="ecotype: Columbia"

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/note="putative s-adenosylmethionine synthetase"

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/db\_xref="GI:14335070"

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1269..1510

BASE COUNT 400 a 310 c 361 g 439 t

## ORIGIN

## Query Match

Best Local Similarity 21.4%; Score 50.4; DB 8; Length 1510;

Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

## REFERENCE

1 (bases 1 to 1510)  
Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Tracy, S.E., Banh, J., Bowser, L., Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,



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VERSION	AC022521.4		PLN 06-SEP-2000
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SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
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AUTHORS	1 (bases 1 to 121668)		
REFERENCE	Federpspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Alatafi,H., Nguyen,M., Lam,B., Southwick,A., Bel,Q., Buehler,E., Buendler,E., Chao,Q., Chin,C., Chou,J., Choi,E., Gonzalez,A., Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M., Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaverl,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 121668)		
AUTHORS	Federpspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Alatafi,H., Nguyen,M., Lam,B., Southwick,A., Bel,Q., Buehler,E., Chin,C., Chou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaverl,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.		
JOURNAL	Submitted (05-FEB-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
TITLE	3 (bases 1 to 121668)		
AUTHORS	Federpspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Alatafi,H., Nguyen,M., Lam,B., Southwick,A., Bel,Q., Buehler,E., Chin,C., Chou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaverl,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.		
JOURNAL	Submitted (15-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
REFERENCE	4 (bases 1 to 121668)		
AUTHORS	Federpspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Alatafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.		
JOURNAL	Submitted (20-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
TITLE	5 (bases 1 to 121668)		
AUTHORS	Federpspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Alatafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.		
JOURNAL	Submitted (06-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
COMMENT	On May 20, 2000 this sequence version replaced gi:7743863. Bases 1-25,600 of clone T14P4 overlap with bases 74,643-100,239 of BAC clone F22D16 (AC009525). e-mail for correspondence: arabseqsequence.stanford.edu Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene		





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RESULT 27
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ACCESSION AF170798
VERSION AF170798.1 GI:5726593
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SOURCE petunia x hybrida.
ORGANISM Petunia x hybrida
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Astidae; euasterids II; Solanales; Solanaceae; Petunia.
REFERENCE
1 (bases 1 to 1539)
AUTHORS Soong,S.C. and To,K.Y.
TITLE Nucleotide Sequence Of A cDNA (AF170798) Encoding Type I
S-Adenosyl-L-Methionine Synthetase From Petunia hybrida.
(JPG99-160)
JOURNAL Plant Physiol. 121 (3), 1053 (1999)
REFERENCE
2 (bases 1 to 1539)
AUTHORS To,K.Y. and Sung,H.C.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1999) Institute of Biocgricultural Sciences,
Academia Sinica, Taipei 11529, Taiwan
FEATURES
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BASE COUNT 409 a 323 c 368 g 439 t
ORIGIN
Query Match 21.2%; Score 49.8; DB 8; Length 1539;
Best Local Similarity 77.9%; Pred. No. 0.00034;
Matches 60; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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Db 1272 GGAAGTTCTCAAGCCC 1288

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REFERENCE
AUTHORS
1 (bases 1 to 1665)
Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Shin,P., Banh,J.,
Bower,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M.,
Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T.,
Satou,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
Arabidopsis cDNA clones
Unpublished
TITLE
2 (bases 1 to 1665)
AUTHORS Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Shin,P., Banh,J.,
Bower,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M.,
Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T.,
Satou,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
Direct Submission
Submitted (31-MAR-2001) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
COMMENT
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.
The Salk, Stanford, PEGC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Shin,P., Chen,H.,
Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Tracy,S.E., Banh,J.,
Bower,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A.,
and Ecker,J.R.
Shin,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
FEATURES
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Matches 60; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 159 caggttcacgaagccgcgcacattggccgtgacgacgcgcgacttaccctg 218
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RESULT 29  
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DEFINITION Arabidopsis thaliana chromosome II section 201 of 255 of the  
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AC006922 AE02093  
VERSION AC006922.6 GI:6598638  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 114950)  
Lin, X., Kaul, S., Rounsley, S.D., Shea, J.P., Benito, M.-I., Town, C.D.,  
Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Rong, C.M.,  
Fel'dbaum, V., Buell, C.R., Ketchum, K.A., Lee, J.-J., Renning, C.M.,  
Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L.,  
Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,  
Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D.,  
Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and  
Venter, J.C.  
TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana  
JOURNAL Nature 402 (6763), 761-768 (1999)  
MEDLINE 20083487  
PUBMED 10617197  
REFERENCE 2 (bases 1 to 114950)  
AUTHORS Lin, X.  
DIRECT SUBMISSION  
SUBMITTED (09-MAR-2000) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA  
On Dec 17, 1999 this sequence version replaced gi:488359.  
The sequence and annotation of chromosome 2 were merged from those  
of the individual clones on this chromosome after removing  
overlaps. For detailed information, please see the TIGR web site  
(http://www.tigr.org/cdb/at.html).

Genes were identified by a combination of three methods: Gene  
prediction programs including GRL  
(ftp://artur.epm.ornl.gov/pub/xyrail), GeneFinder (Phil Green,  
University of Washington), Genscan (Chris Burge,  
http://genomic.stanford.edu/GENSCAN.html), and NetPlantGene  
(http://www.cbs.dtu.dk/services/NetGene2/), searches of the  
complete sequence against a peptide database and plant EST  
databases at TIGR, and manual curation based on those analyses.  
Annotated genes are named to indicate the level of evidence for  
their annotation. Genes with similarity to other proteins are named  
after the database hits. Genes without significant peptide  
similarity but with EST similarity are named as 'unknown' proteins.  
Genes without protein or EST similarity, that are predicted by two  
or more gene prediction programs over most of their length are  
annotated as 'hypothetical' proteins. Genes encoding tRNAs are  
predicted by tRNAscan-SE (Sean Eddy,  
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were  
identified by RepeatMasker (Arian Smit,  
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are  
numbered from the top to bottom of the chromosome.

database support.  
This work was supported by the National Science Foundation,  
Department of Energy and the US Department of Agriculture.

Address all correspondence to: atetigr.org.  
Location/Qualifiers  
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We thank the CSHL/Mashu/ABI consortium for sequencing BAC clones  
F6P23, F5J6, T17A5, and T13JL6, the ESSA group for sequencing clone  
F1J3D, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards  
and Satoshi Tabata for helpful assistance. In addition, we would  
like to thank the TIGR Bioinformatics Department, especially Dixin  
Zhou, Hanif Khaliq, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy  
Peterson, Michael Holmes, and Delwood Richardson for software and

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RESULT 30  
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DEFINITION Solanum tuberosum S-adenosylmethionine synthetase mRNA, partial  
cds.  
ACCESSION AF443869  
VERSION AF443869.1 GI:17226671  
KEYWORDS  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; easterids I; Solanales; Solanaceae; Solanum.

REFERENCE  
AUTHORS Ambrosino, P., Bosco, A. and Ruocco, M.  
TITLE S-adenosylmethionine synthetase from potato  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Ambrosino, P., Bosco, A. and Ruocco, M.  
TITLE Submitted (06-NOV-2001) At. Bo. Pa. Ve, University, Via Universite,  
100, Portici, NA 80055, Italy  
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QY 219 cgaggtgtgtaagcccc 235  
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RESULT 31  
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DEFINITION L.esculentum S-adenosyl-L-methionine synthetase mRNA, complete cds.  
ACCESSION 224741  
VERSION 224741.1 GI:429103  
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SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; easterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
REFERENCE 1 (bases 1 to 1479)  
AUTHORS Espartero, J. and Pardo, J.M.  
TITLE Differential expression of three S-adenosylmethionine synthetase  
genes in response to stress in tomato  
JOURNAL Unpublished

TITLE	JOURNAL
Direct Submission Submitted (18-APR-1996) Schroeder J., University of Freiburg, Institut fuer Biologie II, Schenkestr. 1, D-79104 Freiburg,	GEMANY
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OY	220 gaggttgtaaacgccccc 235 
Dd	1200 GAGGTAGTTTAAGCCCC 1215
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LOCUS	A.thaliana S-adenosylmethionine synthetase gene, complete cds.
DEFINITION	M55077
ACCSSION	M55077.1 GI:166871
KERSTION	S-adenosylmethionine synthetase.
SOURCE	Arabidopsis thaliana DNA.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 2559) Pellemann,J., Boerjan,W., Engler,G., Seurinck,J., Botterman,J., Allioete,T., Van Montagu,M.M. and Inze,D. Strong cellular preference in the expression of a housekeeping gene of Arabidopsis thaliana encoding S-adenosylmethionine synthetase Plant Cell 1, 81-93 (1989)
FEATURES	Location/Qualifiers
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Qy 159 caggttcacaaagccgcatacaggcaacttggccggtcacgaaccgacctacctg 218  
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Db 1065 GCAAGTGGTGAAGCCCTC 1081

RESULT 38  
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LOCUS L.esculentum S-adenosyl-L-methionine synthetase mRNA, complete CDS.  
DEFINITION Z24743  
Z24743 GI:429107  
VERSION 224743.1  
KEYWORDS S-adenosyl-L-methionine synthetase.  
SOURCE tomato.

ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.

REFERENCE 1 (bases 1 to 1455)  
AUTHORS Espartero,J., Pintor-Toro,J.A. and Pardo,J.M.  
TITLE Differential accumulation of S-adenosylmethionine synthetase transcripts in response to salt stress  
JOURNAL MEDLINE Plant Mol. Biol. 25 (2), 217-227 (1994)

MEDLINE 94289646  
REFERENCE 2 (bases 1 to 1455)  
AUTHORS Pardo,J.M.  
TITLE Direct Submission  
JOURNALS Submitted (23-JUL-1993) Jose M. Pardo, Instituto de Recursos Naturales y Agrobiologia,, C.S.I.C., Avda. Reina Mercedes, Sevilla,  
Sevilla, 41080, Spain

FEATURES SOURCE Location/Qualifiers  
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/organism="Lycopersicon esculentum"  
/cultivar="Rutgers"  
/db\_xref="taxon:4081"  
/clone="SAM3"  
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				Gaps 0;

Query Match	20.5%	Score 48.2	DB 8	Length 1565
Best local Similarity	76.6%	Pred. No. 0	001	
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			Gaps	0
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Db 1140	CAGGTCACCAAGAAACTCTCACCATTATGTCTACTTGGCCCGATGATCACCCCGATTACACTG	1199		
QY 219	cgaagtggtcaagccccc	235		
Tb 1200	GGAGACTGTCGAAGTCC	1216		

[illegible]

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Query Match	20.1%; Score 47.2; DB 8; Length 4459;		
Best Local Similarity	76.3%; Fred. No. 0.0022;		
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OY	220 gaggtcgatcaagccccc 235		
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RESULT 44			
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DEFINITION	Chlamydomonas reinhardtii S-adenosylmethionine synthetase (CHRSAMS)		
ACCESSION	AF008568		
VERSION	AF008568		
KEYWORDS	AF008568.1 GI:2454483		
SOURCE			
ORGANISM	Chlamydomonas reinhardtii.		
	Chlamydomonas reinhardtii.		
	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;		
	Chlamydomonadaceae; Chlamydomonas.		
REFERENCE	1 (bases 1 to 820)		
AUTHORS	Kim,J.Y., Lee,K.O. and Lee,S.H.		
JOURNAL	Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase		
REFERENCE	2 (bases 1 to 820)		
AUTHORS	Kim,J.Y., Lee,K.O. and Lee,S.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUN-1997) Biology, Yonsei University, Sinchon-dong		
	134, Seodaemun-gu, Seoul 120-749, Korea		
FEATURES	Location/Qualifiers		
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	0; Mismatches 15; Indels 0; Gaps 0;			
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Db 458	ggtaccagaaagaccgcttagcgccacttggccgcgacatcccgacttcacttcgg	517		
Qy 221	aggtggtcaag	231		
Db 518	agaccgtgaag	528		
RESULT 45				
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LOCUS	Elaeagnus umbellata S-adenosyl-L-methionine synthetase (SAMS1)			
DEFINITION	AF346305	complete cds.		
ACCESSION	AF346305			
VERSION	AF346305.1	GI:13540315		
KEYWORDS				
SOURCE	Elaeagnus umbellata.			
ORGANISM	Elaeagnus umbellata.			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eurosids I; Rosales; Elaeagnaceae; Elaeagnus.			
REFERENCE	1 (bases 1 to 1572)			
AUTHORS	Lee,S.H. and An,C.S.			
TITLE	Structures and expression patterns of two cDNA clones encoding S-adenosyl-L-methionine synthetase from the root nodule of Elaeagnus umbellata			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1572)			
AUTHORS	Lee,S.H. and An,C.S.			
TITLE	Direct Submission			
JOURNAL	Submitted (06-FEB-2001) School of Biological Sciences, Seoul National University, Seoul 151-742, Korea			
FEATURES	Location/Qualifiers			
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BASE COUNT	425 a	333 c	369 g	445 t
ORIGIN				
Query Match	19.8%;	Score 46.6;	DB 8;	Length 1572;
Best Local Similarity	75.3%;	Pred. No. 0.0031;		
Matches 58; Conservative	0; Mismatches 19; Indels 0; Gaps 0;			



Tue Aug 20 07:55:44 2002

us-09-198-779b-1.rge

Page 25

QY	159	caagttcatcaagaacgcgcgcacabagggccactttgycgctgacgcgcgaactcaactg	218
Db	1162	CAGGTCCTCTTAACACGACGACGAGGTATGGACACTTTGGAAGAGATGACCCAGACTTCACATG	1221
QY	219	cgaaagtgtgtcaagcccc	235
Db	1222	GGAGATTGTGAAGCCCC	1238

Search completed: August 20, 2002, 01:29:07  
Job time: 7896 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 23:16:15 ; Search time 1800.16 Seconds  
(without alignments)  
1761.946 Million cell updates/sec

Title: US-09-198-779B-1

Perfect score: 235  
Sequence: 1 gtttcgctagcctcgtg.....ctgcgaggtgtgtcaagcccc 235

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estha:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estinu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_hiv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	122	51.9	512	10	BM075638
3	122	51.9	555	10	BM267205
4	122	51.9	594	10	BM334082
5	122	51.9	650	10	BM339093
6	122	51.9	746	10	BM267021
7	121	51.5	528	9	AI948255
8	121	51.5	554	9	AI795380
9	121	51.5	554	9	AM000206
10	121	51.5	583	9	AM067167
11	121	51.5	605	9	AI855043
12	121	51.5	626	10	BM078637
13	121	51.5	670	10	BM074388
14	120.4	51.2	513	10	BM332958
15	120.4	51.2	609	10	BM347524
16	120.4	51.2	645	10	BM339768
17	120.4	51.2	745	10	BM268790

C 18	119	50.6	548	10	BM348643	BM348643	MEST294-C
C 19	117	49.8	595	9	AI691859	AI691859	606011C12
C 20	110	46.8	752	10	BM336997	BM336997	MEST201-H
C 21	107.6	45.8	637	10	BM079570	BM079570	MEST96-DL
C 22	107.4	45.7	492	9	AM497500	AM497500	660052H09
C 23	103.8	44.2	530	10	BM079887	BM079887	MEST101-A
C 24	100.4	42.7	435	10	BM336874	BM336874	MEST200-A
C 25	100	42.6	533	10	BM336766	BM336766	MEST198-F
C 26	100	42.6	627	9	AI861345	AI861345	614012F08
C 27	100	42.6	648	10	BM350900	BM350900	MEST170-D
C 28	98	41.7	409	9	AI901593	AI901593	618007E09
C 29	85	36.2	581	9	AI714565	AI714565	605059E11
C 30	82	34.9	411	9	AI978238	AI978238	614042B09
C 31	76.8	32.7	499	10	BG550027	BG550027	947080E01
C 32	76.8	32.7	502	10	BG549665	BG549665	947080E01
C 33	76.8	32.7	503	10	BG549664	BG549664	947080E01
C 34	76.2	32.4	602	9	AI657373	AI657373	486053H12
C 35	75.6	32.2	433	10	BI388940	BI388940	949047F08
C 36	75.6	32.2	463	9	AI738382	AI738382	606049C06
C 37	75.6	32.2	490	10	BG550028	BG550028	947080E01
C 38	75.6	32.2	504	10	BE511080	BE511080	946057F06
C 39	75.6	32.2	554	9	AI737785	AI737785	606041C09
C 40	75.6	32.2	581	9	AI734421	AI734421	606031B05
C 41	75.6	32.2	588	9	AI734316	AI734316	606029E07
C 42	75.6	32.2	589	9	AI737411	AI737411	606040B05
C 43	75.6	32.2	591	10	BE511079	BE511079	946057F06
C 44	75.6	32.2	632	9	AM062087	AM062087	660099F01
C 45	75.4	32.1	414	9	AI920328	AI920328	603019C04

#### ALIGNMENTS

RESULT 1  
BM340942/c 232 bp mRNA linear EST 16-JAN-2002  
LOCUS MEST328-A09.T3 ISGM5-RN Zea mays cDNA clone MEST328-A09 3', mRNA  
DEFINITION sequence.  
ACCESSION BM340942  
VERSION BM340942.1 GI:181711102  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 232)  
Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.  
Expressed Sequence Tags from B73 Maize: various stages and tissues  
including seedlings treated with a variety of hormones  
Unpublished (2001)  
Contact: Patrick S. Schnable  
Schnable Laboratory  
Iowa State University  
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu  
Individual basecall and confidence value were assigned using the  
phred software,  
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>  
rt). Overall sequence quality assessment and vector trimming were  
conducted using the lucy software (<http://www.tigr.org/softlib/lucy/>).  
Lucy parameters were set to ensure an overall trimmed quality of  
97.5% or better without any vector fragments in the chosen  
high-quality region of each sequence. Low-quality bases between the  
poly-T and the high-quality region were replaced with N's to serve  
as spacers.  
PCR Primers  
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)  
BACKWARD: primer T7-2 (ATT AAC CCA CAC TAA AG)  
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).  
Location/Qualifiers

#### FEATURES



[illegible]

Iowa State University  
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA  
Tel: 515-294-0975  
Tel: 515-294-2289  
Fax: 515-294-2289  
Email: schmale@iastate.edu

Individual Basecall and confidence value were assigned using the  
phred software,  
([#http://depts.washington.edu/ventures/collabtr/direct/index.htm](http://depts.washington.edu/ventures/collabtr/direct/index.htm);  
rt). Overall sequence quality assessment and vector trimming were  
conducted using the lincy software (<http://www.tlgr.org/soflab/>)  
Lucy parameters were set to ensure an overall trimmed quality of  
97.5% or better without any vector fragments in the chosen  
high-quality region of each sequence. Low-quality bases between the  
poly-T and the high-quality region were replaced with N's to serve  
as spacers.

PCR primers  
FORWARD: primer T7-1 (NA TAC GAC TCA CTA TAG)  
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)  
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers  
1..555

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Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (11, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG)
7, Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings,
NMA (alpha-Naphthalene acetic acid)-treated seedlings,
Kinetin-treated seedlings, ACPG
1-aminocyclopropane-1-carboxylic acid)-treated seedlings
Brassinolide-treated seedlings, ABA (Abscissic acid
)-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5

```

AACGCGAAGAAATTTCGCGCCGACAGAAATTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol- $\alpha$ -catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cor value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

[illegible]

RESULT	4
LOCUS	BM334082/c
DEFINITION	BM334082 MEST132-C11.T3 ISUM5-RN Zea mays cDNA clone MEST132-C11 3', mRNA
ACCESSION	Sequence.
VERSION	BM334082
KEYWORDS	BM334082.1 GI:18164243
SOURCE	EST.
ORGANISM	Zea mays. Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 594) Went,T.J., Qiu,F., Guo,L., Ashrock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various strages and tissues including seedlings treated with a variety of hormones Unpublished (2001) Contact: Patrick S. Schnable
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Individual baseness and confidence value were assigned using the phred software,  
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>>http://depts.washington.edu/ventures/collabtr/direct/index.htm>). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/soflab/>>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.

PCR Primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)  
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)  
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers

1..594  
/organism="Zea mays"

Schnable Laboratory  
Iowa State University  
G405 Agronomy, Iowa State University,  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu  
Individual basecall and confidence value were assigned using the  
phred software,  
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>>#th  
rt). Overall sequence quality assessment and vector trimming were  
conducted using the Lucy software (<http://www.tigr.org/software/>).  
Lucy parameters were set to ensure an overall trimmed quality of  
97.5% or better without any vector fragments in the chosen  
high-quality region of each sequence. Low-quality bases between the  
poly-T and the high-quality region were replaced with N's to serve  
as spacers.  
PCR Primers  
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)  
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)  
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).  
Location/Qualifiers  
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Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),  
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels  
(3, 5, 10, 15, 20, 25, 30, DAG), Adventitious roots (65 DAG  
, Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0  
DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0

[illegible]

RESULT	5
LOCUS	BM339093/c
DEFINITION	BM339093
ACCESSION	MEST226-F10.T3 ISUM5-RN zea mays mRNA linear EST 16-JAN-2002
VERSION	sequence.
KEYWORDS	BM339093
SOURCE	BM339093.1 GI:18169253
ORGANISM	zea mays. zeo mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 650)
REFERENCE	Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones Unpublished (2001) Contact: Patrick S. Schnable
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

[illegible]



```

OY 1 gtttcgctacgctcgtgagacagatcgacgctgcccacatgctgataatgagcgctcc 60
    |||||||
Db 124 GTTTCCGCTACCGCTCGGAGACATCGACCTGCCCTGCTGATTAATGGAGCGCTCC 65
    |||||||
OY 61 tgatccatgctcgtgctgtatataatgtgtataatgagcagagacacacgctacgt 120
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OY 121 t 121
    |
Db 4 T 4

RESULT 8
LOCUS AI795380 554 bp mRNA linear EST 02-JUL-1999
DEFINITION 614009A12.x2 614 - root cDNA library from Walbot Lab Zea mays cDNA,
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ACCESSION AI795380
VERSION AI795380.1 GI:5343195
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 554)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
    University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
    Department of Biological Sciences
    Stanford University
    855 California Ave, Palo Alto, CA 94304, USA
    Tel: 650 723 2227
    Fax: 650 725 8221
    Email: walbot@stanford.edu
    Plate: 614009 row: A column: 12.
FEATURES
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            /cultivar="W23"
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            /lab_host="XLDLR"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2,8e-24;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

AM000206
LOCUS AM000206 554 bp mRNA linear EST 08-SEP-1999
DEFINITION 614009A12.Y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
    mRNA sequence.
ACCESSION AM000206
VERSION AM000206.1 GI:5847127
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 554)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
    University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
    Department of Biological Sciences
    Stanford University
    855 California Ave, Palo Alto, CA 94304, USA
    Tel: 650 723 2227
    Fax: 650 725 8221
    Email: walbot@stanford.edu
    Plate: 614009 row: A column: 12.
FEATURES
    source
        1..554
            /organism="Zea mays"
            /cultivar="W23"
            /db_xref="taxon:4577"
            /clone_lib="614 - root cDNA library from Walbot Lab"
            /tissue_type="root"
            /dev_stage="3-4 days old"
            /lab_host="XLDLR"
            /note="Organ: root; Vector: pBluescriptII SK+; Site_1:
            EcotRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
            Lab (LM)"
BASE COUNT 149 a 128 c 128 g 149 t
ORIGIN
Query Match 51.5%; Score 121; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 2,8e-24;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 683016 row: F column: 05.

FEATURES  
source  
1. 583  
/organism="Zea mays"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="683 - 14 day immature embryo from Hake lab (HS)"  
/tissue\_type="embryo"  
/dev\_stage="14 days after pollination"  
/lab\_host="DH10B"  
/note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap Express); Site\_1: XhoI; Site\_2: EcoRI; Directionally cloned, 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."

BASE COUNT 155 a 135 c 131 g 162 t

ORIGIN

Query Match 51.5%; Score 121; DB 9; Length 583;  
Best Local Similarity 100.0%; Pred. No. 2.8e-24;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcttcgctagcctggtgagacagatcgacgctgcccacgtcgataatgagacgctc 60  
|||||  
DB 145 GTTTCGCTAGCCTCGTGACAGATCGACGCTGCCATGCTGATTAATGAGACGGTCC 86  
|||||  
OY 61 tgaaccattgtctgtgtatcaatgtgtataatgacagacacacacgtact 120  
|||||  
DB 85 TGATCCATTGTCGTGTGTTATTAATGTTGTTATTAATGACGACGACACGCTACT 26  
|||||  
OY 121 t 121  
+  
DB 25 T 25

RESULT 11  
A1855043/c 605 bp mRNA linear EST 02-FEB-2000  
LOCUS 606074C08.x1 606 - Ear tissue cDNA library from Schmidt lab Zea  
DEFINITION mays cDNA, mRNA sequence.  
ACCESSION A1855043  
VERSION A1855043.1 GI:5499176  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 605)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 606074 row: C column: 08.  
Location/Qualifiers

source  
1. 605  
/organism="Zea mays"  
/cultivar="Ohio43"  
/db\_xref="taxon:4577"  
/clone\_lib="606 - Ear tissue cDNA library from Schmidt lab"  
/tissue\_type="mixed"  
/dev\_stage="ear length from 0.5 cm - 2.0 cm"  
/lab\_host="XLOLR (Stratagene)"  
/note="Organ: Immature ear; Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"

BASE COUNT 161 a 145 c 136 g 163 t

ORIGIN

Query Match 51.5%; Score 121; DB 9; Length 605;  
Best Local Similarity 100.0%; Pred. No. 2.8e-24;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcttcgctagcctggtgagacagatcgacgctgcccacgtcgataatgagacgctc 60  
|||||  
DB 145 GTTTCGCTAGCCTCGTGACAGATCGACGCTGCCATGCTGATTAATGAGACGGTCC 86  
|||||  
OY 61 tgaaccattgtctgtgtatcaatgtgtataatgacagacacacacgtact 120  
|||||  
DB 85 TGATCCATTGTCGTGTGTTATTAATGTTGTTATTAATGACGACGACACGCTACT 26  
|||||  
OY 121 t 121  
+  
DB 25 T 25

RESULT 12  
BM078637/c 626 bp mRNA linear EST 14-NOV-2001  
LOCUS MEST122-D04.T3 ISD04-TN Zea mays cDNA clone MEST122-D04 3', mRNA  
DEFINITION sequence.  
ACCESSION BM078637  
VERSION BM078637.1 GI:16925569  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 626)  
Qiu, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.  
Expressed Sequence Tags from B73 Maize Seedlings and Silks  
Unpublished (2001)  
Contact: Patrick S. Schnable  
Schnable Laboratory  
Iowa State University  
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu  
Individual basecall and confidence value were assigned using the  
phred software,  
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>;  
rt). Overall sequence quality assessment and vector trimming were  
conducted using the Lucy software (<http://www.tigr.org/softlab/lucy/>).  
Lucy parameters were set to ensure an overall trimmed quality of  
97.5% or better without any vector fragments in the chosen  
high-quality region of each sequence. Low-quality bases between the  
poly-A and the high-quality region were replaced with N's to serve  
as spacers.  
PCR Primers  
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA  
CTA TAG)  
BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC  
TAA AG)  
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers  
1. .626

Query Match	51.5%;	Score 121;	DB 10;	Length 626;
Best Local Similarity	100.0%;	Pred. No. 2.9e-24;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 13  
BM074388/C

ACCESSION	BM074388
VERSION	BM074388.1
GI	GI:16919855

Zea mays.  
Zea mays

**AUTHORS** QU, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T. J. and Schnable, P.S.  
**TITLE** Expressed Sequence Tags from B73 Maize Seedlings and Silks  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Patrick S. Schnable

Individual basecall and confidence value were assigned using the phred software, (<http://depts.washington.edu/ventures/collabtr/direct/index.htm#btr>). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/softlab/>).

Location/Qualifiers  
1. .670

Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.

PCR Primers

FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

BASE COUNT  
ORIGIN

173 a 158 c 150 g 178 t 11 others

```

/c/clone_1mb103-ELU"
/c/clone_1lb="150M4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/notes="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5',
AAGTCGACGACATTCGCGCGCCGCGACGAGATTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
was went through one round of normalisation to COT value
of 5 based on the methods of Marcello Bento Soares (Genome
Research 6: 791-806, 1996)."

```

Query Match	51.5%	Score 121	DB 10	length 670
Best Local Similarity	100.0%	Pred. No.	2.9e-24	
Matches 121	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

Qy	1	gtttccgcctagcctcgttgaaagctgaacgctcccaatcgtataaataagaaagctc	60
Db	151	gTTTTCCGCTAAGCCTCGGTGGAGACAGTCCACGCTGCCATGCTGTAATATGACGGTCC	92
Qy	61	tgatccatcgttcgtctgtatataatgtgtataatctagacagagacacaacacgtacgt	120
Db	91	TCATCATCTGGTCGTTGGTATTAATAGTGTTAATTAATGAGCAGAGCACAACAGTAGGT	32

QY	121	t	121
		1	
Db	31	T	31

RESULT 14  
BM332958/c

LOCUS	513 bp
BM332958	mRNA
DEFINITION	linear EST 16-JAN-2002
	ME81182-A04.T3 ISUM5-RN Zea mays cDNA clone ME81182-A04 3', mRNA sequence..
ACCESSION	BM332958
VERSION	BM332958.1
	GI:18163119

SOURCE ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 513)  
Men, T. J., Qiu, F., Guo, L., Ashlock, D. A. and Schnable, P. S.  
Expressed Sequence Tags from B73 Maize: various stages and tissues  
including seedlings treated with a variety of hormones  
Unpublished (2001)









```

/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST96-D10"
/clone_lib="ISUM4-TN"

```

```

BASE COUNT      134 a      115 c      110 g      133 t
                /note="Organ: Anthr; Vector: Lambda Zap; Site_1: Eco
                Site_2: XhoI; Anthr and pollen cDNA library.
                Directionally sequenced with 5' end at the EcoRI site
                Created by Amie Franklin."

```



## ORIGIN

Query Match 45.7%; Score 107.4; DB 9; Length 492;  
 Best Local Similarity 98.3%; Pred. No. 2e-20;  
 Matches 119; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtttcgcgtacgctcgtgagacagatcgaacgtccatgctgataatgagcgttc 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 141 GTTTCGCTACGCTCGGTGAGACAGATCAGCTCCCTGCTGATTAATGACGCTCC 82  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 tgaatcattgctcgtgtgtatataatgtgtataattgagcagacacacagctagt 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 81 TGATTCATTGCTGCTGTGTATTATTAATGATGCA-CAGGACACACAGCTAGCT 23  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 t 121  
 |  
 Db 22 T 22

## RESULT 23

BM079887/c

LOCUS BM079887 530 bp mRNA linear EST 14-NOV-2001  
 DEFINITION MEST101-A03.T3 ISUM4-TN Zea mays cDNA clone MEST101-A03 3', mRNA  
 sequence.

## ACCESSION

BM079887

VERSION BM079887.1 GI:16926819

## KEYWORDS

EST.

## SOURCE

Zea mays.

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## REFERENCE

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

## AUTHORS

Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.

## TITLE

Expressed Sequence Tags from B73 Maize Seedlings and Silks

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the

phred software,

&lt;http://depts.washington.edu/ventures/collabtr/direct/index.htm#b

rt&gt;. Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (&lt;http://www.tigr.org/softlab/&gt;).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve

as spacers.

PCR Primers

FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA

CTA TAG)

BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC

TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers

1..530

/organism="Zea mays"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone="MEST101-A03"

/clone\_1id="ISUM4-TN"

/tissue\_type="Seedling and silk"

/lab\_host="DH10B"

/note="Vector: pT73PAC; Site\_1: EcoRI; Site\_2: NotI;  
 ds-cDNA molecules were generated as follows. First-strand  
 cDNA was prepared from oligo-dT selected mRNA by priming  
 with a NotI oligo-dT primer (5',

## BASE COUNT

144 a 124 c 121 g 141 t

Query Match 44.2%; Score 103.8; DB 10; Length 530;  
 Best Local Similarity 96.7%; Pred. No. 2.2e-19;  
 Matches 117; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 gtttcgcgtacgctcgtgagacagatcgaacgtccatgctgataatgagcgttc 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 142 GTTTCGCTACGCTCGGTGAGACAGATCAGCTCCCTGCTGATTAATGACGCTCC 83  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 tgaatcattgctcgtgtgtatataatgtgtataattgagcagacacacagctagt 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 82 TGATTCATTGCTGCTGTGTATTATTAATGTTG--ATTATGACAGACACACAGCTAGCT 25  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 t 121  
 |  
 Db 24 T 24

## RESULT 24

BM336874/c

LOCUS BM336874 435 bp mRNA linear EST 16-JAN-2002

DEFINITION MEST200-A08.T3 ISUM5-RN Zea mays cDNA clone MEST200-A08 3', mRNA

sequence.

ACCESSION BM336874

VERSION BM336874.1 GI:18167035

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade: Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 435)

Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A. and Schnable,P.S.

Expressed Sequence Tags from B73 Maize: various stages and tissues

including seedlings treated with a variety of hormones

unpublished (2001)

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the

phred software,

&lt;http://depts.washington.edu/ventures/collabtr/direct/index.htm#b

rt&gt;. Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (&lt;http://www.tigr.org/softlab/&gt;).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve

as spacers.

PCR Primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers

1..435

/organism="Zea mays"



```

/cultivar="B73"
/db.xref="taxon:4577"
/clone="MEST200-A08"
/clone_lib="ISUM5-RN"
/issue_type="mixed"
/lab_host="DH10B"
/Note="Vector: pRT3PAC; Site.1: EcoRI; Site.2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings
, NAA (a-Naphthalene acetic acid)-treated seedlings,
Kinetin-treated seedlings, ACP
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscissic acid
)-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
AACTGGAAGAATTGCGCGCCGACGAAATTTTATTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pRT3PAC vector. The library
then went through one round of normalization to Cor value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996). "
BASE COUNT      116 a      104 c      86 g      108 t      21 others
ORIGIN

Query Match      42.7%; Score 100.4; DB 10; Length 435;
Best Local Similarity 72.3%; Pred. No. 2e-18;
Matches 115; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

Oy 1 gtttcgctcagcctcgtgtgacagatcgacgctccatcgtataataatgacgctc 60
|||||
Db 213 GTTTCCGCTAGCAT-AAGACACAGATCGACACGCGCCATGCTGATTAATGAGCGGCC 155
|||||

Oy 61 tgaatccatgttcgtgtgtatataatgttgacgagacacacacgtaagt 120
|||||
Db 154 TGATCCATTGTTGCTGTGTTATTAATGTTGATTAATGAGACACACACGCTAGCT 95
|||||

Oy 121 tnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 159
|
Db 94 TACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 56
|

RESULT 25
BM336766 533 bp mRNA linear EST 16-JAN-2002
LOCUS MEST198-F01.T3 ISUM5-RN Zea mays cDNA clone MEST198-F01 3', mRNA
DEFINITION sequence.
ACCESSION BM336766
VERSION BM336766
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 533)
AUTHORS Wen.T.J., Qiu.F., Guo.L., Ashlock.D.A and Schnable.P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable

```

```

Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the
phred software,
(<http://depts.washington.edu/ventures/collabr/direct/index.htm#b
rt>). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/software/lucy/
>). Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES
Source
Location/Qualifiers
1..533
/organism="Zea mays"
/cultivar="B73"
/db.xref="taxon:4577"
/clone="MEST198-F01"
/clone_lib="ISUM5-RN"
/issue_type="mixed"
/lab_host="DH10B"
/Note="Vector: pRT3PAC; Site.1: EcoRI; Site.2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings
, NAA (a-Naphthalene acetic acid)-treated seedlings,
Kinetin-treated seedlings, ACP
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscissic acid
)-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
AACTGGAAGAATTGCGCGCCGACGAAATTTTATTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pRT3PAC vector. The library
then went through one round of normalization to Cor value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996). "

```

```

BASE COUNT      147 a      121 c      114 g      143 t      8 others
ORIGIN

Query Match      42.6%; Score 100; DB 10; Length 533;
Best Local Similarity 95.0%; Pred. No. 2.7e-18;
Matches 114; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Oy 1 gtttcgctcagcctcgtgtgacagatcgacgctccatcgtataataatgacgctc 60
|||||
Db 209 GTTTCCGCTAGCCTAAGAAAACAGATCGACGCGCCATGCTGATTAATGAGCGGCC 150
|||||

Oy 61 tgaatccatgttcgtgtgtatataatgttgacgagacacacacgtaagt 120
|||||
Db 149 TGATCCATTGTTGCTGTGTTATTAATGTTG-ATTAATGAGACACACACGCTAGCT 91
|||||

```

```

RESULT 26
LOCUS   A1861345/c
DEFINITION 627 bp mRNA linear EST 19-JUL-1999
          mRNA sequence.
ACCESSION A1861345
VERSION   A1861345.1 GI:5525452
KEYWORDS  EST.
SOURCE    Zea mays.
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 627)
REFERENCE
AUTHORS   Maize ESTs from various cDNA libraries sequenced at Stanford
TITLE      University
JOURNAL    Unpublished (1999)
COMMENT    Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 614012 row: F column: 08.
FEATURES
Source
    1..627
    /organism="Zea mays"
    /cultivar="W23"
    /db_xref="taxon:4577"
    /clone_lib="614 - root cDNA library from Walbot Lab"
    /tissue_type="root"
    /dev_stage="3-4 days old"
    /lab_host="XLOLR"
    /note="Organ: root; Vector: pBluescriptII SK+; Site:1:
    EcorI; Site_2: XhoI; 3-4 days old root tissue from Walbot
    Lab (LM)"
BASE COUNT 174 a 154 c 146 g 153 t
ORIGIN
Query Match 42.6%; Score 100; DB 9; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gtttcgctacgctcggtgacagatgcacgtctgcccattgataatgacgtcc 60
    |||||||
Db 103 gttttccgtacgctcggtgacagatgcacgtctgcccattgataatgacgtcc 44
Oy 61 tgatcattgttcgtgtgtatataatgttataatga 100
    |||||||
Db 43 tgatcattgttcgtgtgtatataatgttataatga 4
RESULT 27
LOCUS   BM350900/c
DEFINITION 648 bp mRNA linear EST 16-JAN-2002
          MEST270-D08.T3 ISUM5-RN Zea mays cDNA clone MEST270-D08 3', mRNA
          sequence.
ACCESSION BM350900
VERSION   BM350900.1 GI:18175671
KEYWORDS  EST.
SOURCE    Zea mays.
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 648)
REFERENCE
AUTHORS   Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
TITLE      Expressed Sequence Tags from B73 Maize: various stages and tissues
          including seedlings treated with a variety of hormones
          Unpublished (2001)
JOURNAL

```

```

COMMENT
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
phred software.
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAC)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES
Source
    1..648
    /organism="Zea mays"
    /cultivar="B73"
    /db_xref="taxon:4577"
    /clone_lib="MEST270-D08"
    /clone_lib="ISUM5-RN"
    /tissue_type="mixed"
    /lab_host="DH10B"
    /note="Vector: pT73PAC; Site_1: EcorI; Site_2: NotI;
    Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
    Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
    (3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
    ), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
    cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
    first ear, ear shank, etiolated seedlings, callus,
    Cycloheximide-treated callus, Anaerobic treated seedlings
    , NMA (a-Naphthalene acetic acid)-treated seedlings,
    Kinetin-treated seedlings, ACPc
    (1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
    Brassinolide-treated seedlings, ABA (Absciscic acid
    )-treated seedlings, GA (Gibberellic acid)-treated
    seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA
    molecules were generated as follows. First-strand cDNA was
    prepared from oligo-dT selected mRNA by priming with a
    NotI oligo-dT primer (5',
    AACTGAGAAATTCGCCGCCGACAGCAATTTTCTTTTCTTTT). The
    resulting DNA:RNA hybrid was treated with RNase H and used
    as a template for DNA Pol-I-catalyzed second strand
    synthesis. After the addition of EcorI adaptors, the
    ds-cDNAs were digested with NotI and size-selected. The
    resulting molecules were directionally cloned into the
    EcorI and NotI sites of the pT73PAC vector. The library
    then went through one round of normalization to Cot value
    of 5 based on the methods of Marcelo Bento Soares (Genome
    Research 6: 791-806, 1996)."
BASE COUNT 182 a 151 c 144 g 171 t
ORIGIN
Query Match 42.6%; Score 100; DB 10; Length 648;
Best Local Similarity 73.0%; Pred. No. 2.9e-18;
Matches 100; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Oy 23 acagatgacgctcccatgctgataatgacgctctgcatcattgttggtgta 82
    |||||||
Db 192 ACAGATGACGCTCCCATGCTGATAATGACGCTCTGATTCATTGTTGTTGTGTTA 133
Oy 83 ttaatgtgataatgacgagacacacgctacgttinnnnnnnnnnnnnnnnnnnn 142
    |||||||
Db 132 TTAATGTTGTTAATGACGAGACACACGCTACGTTACTCTCTGTGTGTGTGTGT 73

```

Qy 143 nnnnnnnnnnnnnnc 159  
 Db 72 TTGCATGCATCTCTC 56

RESULT 28  
 AI901593 409 bp mRNA linear EST 27-JUL-1999  
 LOCUS AI901593/c  
 DEFINITION 618007E09.x1 618 - Inbred Tassel cDNA Library Zea mays cDNA, mRNA  
 sequence.  
 ACCESSION AI901593  
 VERSION AI901593  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.

REFERENCE  
 AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 618007 row: E column: 09.  
 location/Qualifiers

FEATURES  
 source 1..409  
 /organism="Zea mays"  
 /cultivar="Ohio43"  
 /db\_xref="taxon:4577"  
 /clone\_lib="618 - Inbred Tassel cDNA Library"  
 /tissue\_type="tassel"  
 /dev\_stage="tassel length from 0.1 to 2.5 cm"  
 /lab\_host="XhoLR"  
 /note="Organ: tassel; Vector: PAD-GAL4-2.1 (Hybridzap);  
 Inbred tassel library from Schmidt lab"

BASE COUNT 120 a 97 c 93 g 99 t

ORIGIN

Query Match 41.7%; Score 98; DB 9; Length 409;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-18;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtctccgtctagcctcgatgacagatcgacgtctgccatcgatgataaattgacggtcc 60  
 |||||||  
 Db 98 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTGCCCATGCTGATTAATGACGGTCC 39  
 |||||||

Qy 61 tgatccattgtcgttgatataatgattgataatt 98  
 |||||||  
 Db 38 TGATCATTGTGCTGCTGTTATTAATGCTGTAATTT 1

RESULT 29  
 AI714565 581 bp mRNA linear EST 02-FEB-2000  
 LOCUS AI714565/c  
 DEFINITION 605059E11.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays  
 cDNA, mRNA sequence.  
 ACCESSION AI714565  
 VERSION AI714565.1 GI:50183772  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.

REFERENCE  
 AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 614042 row: B column: 09.  
 location/Qualifiers

FEATURES  
 source 1..411  
 /organism="Zea mays"  
 /cultivar="W23"  
 /db\_xref="taxon:4577"  
 /clone\_lib="614 - root cDNA library from Walbot lab"

AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 605059 row: E column: 11.  
 location/Qualifiers

FEATURES  
 source 1..581  
 /organism="Zea mays"  
 /cultivar="Ohio43"  
 /db\_xref="taxon:4577"  
 /clone\_lib="605 - Endosperm cDNA library from Schmidt lab"  
 /tissue\_type="nucellar, embryo, and endosperm"  
 /dev\_stage="10-14 days post-pollination"  
 /lab\_host="DH5(alpha)"  
 /note="Organ: kernel; Vector: PAD-GAL4-2'; Site\_1: EcoRI;  
 Site\_2: XhoI; kernel endosperm cDNA library from Schmidt  
 lab"

BASE COUNT 155 a 148 c 138 g 140 t

ORIGIN

Query Match 36.2%; Score 85; DB 9; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-14;  
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtctccgtctagcctcgatgacagatcgacgtctgccatcgatgataaattgacggtcc 60  
 |||||||  
 Db 85 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTGCCCATGCTGATTAATGACGGTCC 26  
 |||||||

Qy 61 tgatccattgtcgttgatataatgattgataatt 85  
 |||||||  
 Db 25 TGATCATTGTGCTGCTGTTATTAATGCTGTAATTT 1

RESULT 30  
 AI978238 411 bp mRNA linear EST 27-AUG-1999  
 LOCUS AI978238/c  
 DEFINITION 614042B09.x2 614 - root cDNA library from Walbot lab Zea mays cDNA,  
 mRNA sequence.  
 ACCESSION AI978238  
 VERSION AI978238.1 GI:5791446  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.

REFERENCE  
 AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 614042 row: B column: 09.  
 location/Qualifiers

FEATURES  
 source 1..411  
 /organism="Zea mays"  
 /cultivar="W23"  
 /db\_xref="taxon:4577"  
 /clone\_lib="614 - root cDNA library from Walbot lab"

[illegible][illegible]

[illegible]

[illegible]

	Db	1	AGGGATGATTCACCACTCACCCTCGACTTCAAGAAGGCCGCACAAGGTTCATCCAAAGACCGC	60
Oy	177	cgcatacggccactttgacgttcagcacgcccgacctcaaccctgtcgaagtgtccaaggccc	235	
Db	61	CGCATTACGGCCCATTTTGCGCGTAGACGAGCCGCGACTTCACTGGAAGGTGTCTAAGCCCC	119	
RESULT	38			
BES11080				
LOCUS			504 bp mRNA linear EST 07-AUG-2000	
DEFINITION			946057F06.y1 946 - tassal primordium prepared by Schmidt lab Zea	
ACCESSION			mays CDNA, mRNA sequence.	
VERSION			BES11080.1 GI:9732328	
KEYWORDS			EST.	
SOURCE			Zea mays.	
ORGANISM			Zea mays.	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC	
			clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE			1 (bases 1 to 504)	
AUTHORS			Walbot,V.	
TITLE			Maze Ests from various cDNA libraries sequenced at Stanford University	
JOURNAL			Unpublished (1999)	
COMMENT			Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave., Palo Alto, CA 94304, USA Tel.: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 946057 row: F column: 06. location/Qualifiers  1..504 /organism="Zea mays" /cultivar="OH43" /db_xref="taxon:4577" /cloned_lib="x946 - tassal primordium prepared by Schmidt lab"	
FEATURES			/tissue_type="tassels" /dev_stage="just after the transition from vegetative to inflorescence development" /lab_host="XLOLR" /note="Organ: tassels; Vector: HybridAP; Site, 1: EcorI; Site,2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridAP. Sample insert size range was 350 bp to 3 Kb with a 1 kb average."	
BASE COUNT			116 a         130 c         144 g         114 t	
ORIGIN				
Query Match			32.2%; Score 75.6; DB 10; Length 504; Best Local Similarly 65.5%; Pred. No. 2.Se-1l; Matches 78; Conservative 0; Mismatches 41; Indels 0; Gaps 0;	
Oy	117	acgttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncaggttcacatcagaaccgc	176	
Db	94	AGGGATGCTCACCATCACTCGACCTCAGAACGGCGGCAGAGTTTCATCAAAGACCGC	153	
Oy	177	cgcatacggccactttgacgttcagcacgcccgacctcaaccctgtcgaagtgtccaaggccc	235	
Db	154	CGCATACGGCCCATTTTGCGCGTAGACGAGCCGCGACTTCACTGGAAGGTGTCTAAGCCCC	212	
RESULT	39			
LOCUS			554 bp mRNA linear EST 02-FEB-2000	
DEFINITION			606041C09.x1 606 - Ear tissue cDNA library from Schmidtlab Zea	
ACCESSION			mays CDNA, mRNA sequence.	
VERSION			Alf37785.1 GI:5069820	

[illegible]

BASE COUNT	155 a	152 c	133 g	148 t
ORIGIN				

RESULT 43  
BE511079/C

152 c 133 g 148 t





```
/tissue_type="seedling"  
/dev_stage="salt stress"  
/lab_host="E. coli XL Gold"  
/note="Organ: root; Vector: pBluescriptII SK(+) XR;  
Seedling stressed root cDNA library from Wang/Bohnert lab"  
BASE COUNT      116 a      115 c      95 g      88 t  
ORIGIN
```

```
Query Match      32.1%; Score 75.4; DB 9; Length 414;  
Best Local Similarity 98.7%; Pred. No. 2.7e-11;  
Matches 76; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 159 caggttcacaaagaccgcgcacatacgcacitggccgtgacgagccgacttcactg 218  
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 413 CAGGTCATCAAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACTG 354  
  
Qy 219 cgaagtggtcaagcccc 235  
    ||||||||||||||||  
Db 353 GGAGGTGTCAAGCCCC 337
```

Search completed: August 20, 2002, 00:55:59  
Job time: 5984 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 00:21:31 ; Search time 275.56 Seconds

(Without alignments)  
1464.200 Million cell updates/sec

Title: US-09-198-779B-1

Perfect score: 235

Sequence: 1 gtttcgcgtcagctcgtcgtt.....ctgcgaggtgtgtcaagcccc 235

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: N.Geneseq\_032802.\*  
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
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15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
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19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	51.5	2061	21	AAA48574
2	75.6	32.2	1674	21	AAC47744
3	65.8	28.0	1380	20	AA07185
4	61.6	26.2	1182	19	AA09143
5	61	26.0	1182	19	AA09141
6	59.4	25.3	1182	19	AA09142
7	54.6	23.2	399	20	AA081128
8	53	22.6	1485	20	AA07184
9	53	22.6	1518	21	AAA51037

10	51	21.7	1582	20	AA07183	Corn S-adenosylmet
11	50.4	21.4	635	21	AA044219	Arabidopsis thalia
12	50.4	21.4	1508	21	AA033986	Arabidopsis thalia
13	50.4	21.4	1521	21	AA045478	Arabidopsis thalia
14	50.4	21.4	1529	21	AA033535	Arabidopsis thalia
15	49.8	21.2	1653	21	AA045944	Arabidopsis thalia
16	49.8	21.2	1654	21	AA035348	Arabidopsis thalia
17	46.6	19.8	1636	22	AA002296	Arabidopsis thalia
18	42.4	18.0	1393	21	AA046421	Arabidopsis thalia
19	42.4	18.0	1395	21	AA033674	Arabidopsis thalia
20	40.2	17.1	1208	15	AA064204	Arabidopsis thalia
21	40.2	17.1	5392	15	AA064201	snac gene encoding
22	40	17.0	4848	24	AA022684	Sequence compislin
23	40	17.0	4848	24	AA022686	Streptomyces fradi
24	39.4	16.8	1693	21	AA075637	Streptomyces fradi
25	39.4	16.8	1693	21	AA056005	Nucleotide sequenc
26	34.6	14.7	56485	21	AA081476	Contig 004 from co
27	34.6	14.7	349980	21	AA021612	N. meningitidis pa
28	34.6	14.7	837096	21	AA081489	N. meningitidis pa
29	34.4	14.6	4403765	22	AA199683	Mycobacterium tube
30	34.4	14.6	4415129	22	AA199682	Mycobacterium tube
31	33	14.0	17512	23	AB009034	Drosophila melanog
32	31.2	13.3	1844	22	AA099804	Human protein enco
33	30.8	13.1	66788	23	AA059515	Propionibacterium
34	30.6	13.0	606	23	AA051580	Pseudomonas aerugi
35	30.6	13.0	657	21	AA081426	Aspergillus oryzae
36	30.2	12.9	566	21	AA085427	Fusarium venenat
37	29.8	12.7	1519	20	AA064373	GABA-gated chlorid
38	29.6	12.6	3550	23	AB009035	Drosophila melanog
39	29.4	12.5	1683	18	AA086246	CDNA encoding mugw
40	29.2	12.4	1557	21	AA049567	Maize M109 protein
41	29.2	12.4	2604	21	AAA48576	CDNA encoding whea
42	29	12.3	1086	23	AB004431	Drosophila melanog
43	29	12.3	1221	22	AA066738	C glutaminum codin
44	29	12.3	1239	16	AA004566	S-adenosylmethioni
45	29	12.3	1344	22	AA071873	Corynebacterium g1

# ALIGNMENTS

RESULT 1	
AAA48574	standard; cDNA; 2061 BP.
ID	AAA48574
XX	XX
AC	AAA48574;
XX	XX
DT	19-SEP-2000 (first entry)
XX	XX
DE	CDNA encoding corn protein phosphatase 2A regulatory subunit A.
XX	XX
KW	Corn: protein phosphatase 2A; protein phosphorylation modulation;
KW	transgenic plant; gene therapy; ss.
XX	XX
OS	Zea mays.
XX	XX
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	56..1820
FT	/*tag- a
FT	/product- "protein phosphatase 2A regulatory
FT	subunit A"
XX	XX
PN	WO200036121-A2.
XX	XX
PD	22-JUN-2000.
XX	XX
PF	15-DEC-1999; 99WO-US29823.
XX	XX
PR	16-DEC-1998; 98US-0112541.
XX	XX
PA	(DUPPO ) DU PONT DE NEMOURS & CO E. I.
XX	XX
PI	Famodu OO, Miao G, Sakai H, Lee J, Rafalski JA, Klein TM;

XX MPI: 2000-431599/37.  
DR P-PSDB: AAY9819.  
XX  
PT Polynucleotides encoding plant protein phosphatase useful for  
PT modulating reversible protein phosphorylation in plants -  
XX  
PS Claim 4; Page 53-54; 73pp; English.  
XX  
CC The present sequence encodes corn protein phosphatase 2A regulatory  
CC subunit A. The sequence was identified in clone p0018.chsuglor.fis of a  
CC CDNA library made from corn ear shoot. BLAST analysis showed that the  
CC present sequence encodes protein phosphatase 2A regulatory subunit A.  
CC The sequence may be used for the recombinant production of the protein  
CC in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in  
CC fermentation culture. The protein may then be used to modulate the  
CC process of reversible protein phosphorylation in plants. It may be used  
CC directly to supplement a plant's own production of the enzyme or to  
CC rectify mutations that result in the expression of inactive protein.  
CC The protein may also be used to test for modulators of protein  
CC phosphorylation which may be used to alter the activity of the enzyme.  
XX  
SQ Sequence 2061 BP; 549 A; 432 C; 498 G; 582 T; 0 other;

Query Match 51.5%; Score 121; DB 21; Length 2061;  
Best Local Similarity 100.0%; Pred.No. 2.2e-31;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtttcgctctagctcgtgtgacagatcagcgtccatgctgataatgacgtcc 60  
Db 1908 gtttcgctctagctcgtgtgacagatcagcgtccatgctgataatgacgtcc 1967  
Oy 61 tgatccatgttcgtgtgtatataatgtgtatataatgagcagacacacgtacgt 120  
Db 1968 tgatccatgttcgtgtgtatataatgtgtatataatgagcagacacacgtacgt 2027  
Oy 121 t 121  
Db 2028 t 2028

RESULT 2  
AAC47744  
ID AAC47744 standard; DNA; 1674 BP.  
XX AAC47744;  
AC 18-OCT-2000 (first entry)  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Zea mays DNA fragment SEQ ID NO: 54954.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.  
XX  
OS Zea mays subsp. mays.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PE 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139482.  
PR 18-JUN-1999; 99US-0139484.  
PR 18-JUN-1999; 99US-0139485.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140605.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142380.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.



DR WPI: 1999-070263/06.  
DR P-PSDB: AAW97744.

XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -  
XX PT encode: dihydrodipicolinate reductase; diaminopimelate epimerase;  
XX PT threonine synthase; threonine deaminase; S-adenosylmethionine  
XX synthetase

PS Claim 47; Page 69-70; 98pp; English.

CC This is the nucleotide sequence of a cDNA contig that codes for  
CC a full-length wheat S-adenosylmethionine synthetase (see AAW97744).  
CC The contig was assembled from clones isolated from wheat kernel,  
CC leaf, seedling and root cDNA libraries and identified by comparison  
CC to public sequence databases using BLAST algorithms. It shows  
CC sequence similarity to the barley enzyme. The invention relates to  
CC new isolated nucleic acid fragments (see AAW97168-85) encoding plant  
CC enzymes (see AAW97727-44) that catalyze steps in the biosynthesis of  
CC lysine, threonine, methionine, cysteine and isoleucine from  
CC aspartate, the enzyme being selected from dihydrodipicolinate reductase,  
CC diaminopimelate epimerase, threonine synthase, threonine deaminase  
CC or S-adenosylmethionine synthetase. The invention also relates to  
CC the construction of a chimeric gene encoding all or a portion of  
CC the biosynthetic pathway enzyme, in sense or antisense orientation,  
CC where expression of the chimeric gene results in production of  
CC altered levels of the enzyme in a transformed host cell.  
CC Overexpression or reduction of expression of genes encoding the  
CC amino acid biosynthetic pathway enzymes in crop plants such as  
CC corn, soybean and wheat can be used to alter levels of the amino  
CC acids in human food and animal feed. Transformed host cells can  
CC also be used to identify compounds that inhibit one of the enzymes.

XX Sequence 1380 BP; 299 A; 430 C; 379 G; 267 T; 5 other;

Query Match 28.0%; Score 65.8; DB 20; Length 1380;  
Best Local Similarity 90.9%; Pred. No. 1.9e-12;  
Matches 70; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 159 caggttcataagaccgcgcataagccacttgcgcgtgacgcgcgaacttacctg 218  
DB 1155 caggttcataagaccgcgcataagccacttgcgcgtgacgcgcgaacttacctg 1214  
OY 219 cgaggtggtcaagcccc 235  
DB 1215 ggaagtggtgaagcccc 1231

#### RESULT 4

AAT99143  
ID AAT99143 standard; cDNA to mRNA; 1182 BP.

AC AAT99143;

DT 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 3 gene.

KM S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;  
KW sam3; ss.

OS Hordeum vulgare.

PN JP09313186-A.

PD 09-DEC-1997.

PF 28-MAY-1996; 96JP-0133406.

PR 28-MAY-1996; 96JP-0133406.

PA (NIOC) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.  
DR P-PSDB: AAW34542.

XX S-adenosyl-methionine synthase gene - useful in producing plants  
XX PT resistant to alkaline soil  
XX PS Claim 6; Page 10-11; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 3 (sam3)  
CC gene. This DNA sequence may be used in a vector to produce plants which  
CC are resistant to alkaline soil.

SO Sequence 1182 BP; 253 A; 368 C; 331 G; 230 T; 0 other;

Query Match 26.2%; Score 61.6; DB 19; Length 1182;  
Best Local Similarity 88.2%; Pred. No. 4.9e-11;  
Matches 67; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 160 aggttcataagaccgcgcataagccacttgcgcgtgacgcgcgaacttacctg 219  
DB 1084 aggttcataagaccgcgcataagccacttgcgcgtgacgcgcgaacttacctg 1143

OY 220 gaggtggtcaagcccc 235  
DB 1144 ggaagtggtgaagcccc 1159

#### RESULT 5

AAT99141  
ID AAT99141 standard; cDNA to mRNA; 1182 BP.

AC AAT99141;

DT 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 1 gene.

KM S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant;  
KW sam1; ss.

OS Hordeum vulgare.

PN JP09313186-A.

PD 09-DEC-1997.

PF 28-MAY-1996; 96JP-0133406.

PR 28-MAY-1996; 96JP-0133406.

PA (NIOC) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.

DR P-PSDB: AAW34540.

XX S-adenosyl-methionine synthase gene - useful in producing plants  
XX PT resistant to alkaline soil

PS Claim 4; Page 8-9; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 1 (sam1)  
CC gene. This DNA sequence may be used in a vector to produce plants which  
CC are resistant to alkaline soil.

SO Sequence 1182 BP; 253 A; 372 C; 324 G; 233 T; 0 other;

Query Match 26.0%; Score 61; DB 19; Length 1182;  
Best Local Similarity 87.0%; Pred. No. 7.8e-11;  
Matches 67; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 159 caggttcataagaccgcgcataagccacttgcgcgtgacgcgcgaacttacctg 218

Db 1083 caggttcatacaagacagctctcactgctcacttggccgcgagatgctgacttaccctg 1142  
 |||  
 QY 219 cgaagtggtcaagccccc 235  
 |||  
 Db 1143 ggaagtggtcaagccccc 1159

## RESULT 6

AAAT99142  
 ID AAT99142 standard; cDNA to mRNA; 1182 BP.

AC AAT99142;

DT 26-MAR-1998 (first entry)

DE S-adenosylmethionine synthase 2 gene.

KW S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant; sam2; ss.

OS Hordeum vulgare.

PN JP09313186-A.

PD 09-DEC-1997.

PF 28-MAY-1996; 96JP-0133406.

PR 28-MAY-1996; 96JP-0133406.

PA (NIOC) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.

DR P-PSDB; AAM34541.

PT S-adenosyl-methionine synthase gene - useful in producing plants resistant to alkaline soil

PS Claim 5; Page 9-10; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 2 (sam2) gene. This DNA sequence may be used in a vector to produce plants which are resistant to alkaline soil.

CC Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

Query Match 25.3%; Score 59.4; DB 19; Length 1182;

Best Local Similarity 85.7%; Pred. No. 2.8e-10;

Matches 66; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 159 caggttcatacaagacagctctcacttggccgcgagatgctgacttaccctg 218  
 |||  
 Db 1083 caggttcatacaagacagctctcacttggccgcgagatgctgacttaccctg 1142

QY 219 cgaagtggtcaagccccc 235  
 |||  
 Db 1143 ggaagtggtcaagccccc 1159

## RESULT 7

AAAX81128  
 ID AAX81128 standard; cDNA; 399 BP.

AC AAX81128;

DT 06-SEP-1999 (first entry)

DE S-adenosyl methionine (SAM) partial cDNA sequence.

KW Senescence-associated receptor-like protein kinase; sak; sam gene; sag; senescence-associated gene; plant senescence; promoter; pharmaceutical;

KW plant maturation; S-adenosyl methionine; flower; fruit development; ss.  
 OS Phaseolus vulgaris.

PN WO929159-A1.

PD 17-JUN-1999.

PF 08-DEC-1998; 98MO-US25799.

PR 08-DEC-1997; 97US-0067898.

PA (VITA-) VITALITY BIOTECHNOLOGIES INC.

PI Gepstein S, Hajnóje T, Rosner A;

DR WPI: 1999-404873/34.

DR P-PSDB; AAY21978.

PT DNA encoding senescence-associated genes for a senescence receptor-like protein kinase

PS Claim 18; Fig 4; 70pp; English.

CC The invention relates to a senescence-associated receptor-like protein kinase (sak) gene. The sak gene is a senescence-associated gene (sag) and is expressed early in the plant senescence process. The sak gene promoter is useful for driving expression of foreign genes having a desired product, such as a pharmaceutical, during the process of plant maturation. The sak gene promoter can be used to drive expression of resistance genes against pathogens or pests during senescence when the plant is particularly susceptible to infection or infestation. The sak gene promoter may also be used to drive expression of a gene encoding an inhibitor of senescence. Plant senescence may be inhibited by use of antisense sak constructs. Over expression of the sag genes, using the sak or sam (S-adenosyl methionine) gene promoters is useful for CC induction of early senescence. This is useful to obtain flower or fruit development prior to specific pest onset, prior to undesirable cross-fertilization from related crops, at a specific time during storage or retail, or to avoid development of plant structures that are not of CC agronomic importance. The present sequence represents a partial cDNA clone of S-adenosyl methionine (SAM).

CC Sequence 399 BP; 108 A; 80 C; 82 G; 129 T; 0 other;

Query Match 23.2%; Score 54.6; DB 20; Length 399;

Best Local Similarity 81.8%; Pred. No. 7.8e-09;

Matches 63; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 159 caggttcatacaagacagctctcacttggccgcgagatgctgacttaccctg 218  
 |||  
 Db 101 caggttcatacaagacagctctcacttggccgcgagatgctgacttaccctg 160

QY 219 cgaagtggtcaagccccc 235  
 |||  
 Db 161 ggaagtggtcaagccccc 177

## RESULT 8

AAAX07184  
 ID AAX07184 standard; cDNA; 1485 BP.

AC AAX07184;

DT 21-MAY-1999 (first entry)

DE soybean S-adenosylmethionine synthetase cDNA clone s2.12b06.

KW S-adenosylmethionine synthetase; soybean; amino acid; lysine; threonine; methionine; cysteine; isoleucine; transgenic plant; crop improvement; food; feedstuff; ss.

OS	Glycine max.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	74..1252
FT		/*tag= a
PN	MO855601-A2.	
XX		
PD	<u>10-DEC-1998</u>	
XX		
PF	05-JUN-1998;	98WO-US11692.
XX		
PR	12-JUN-1997;	97US-0049443.
XX	06-JUN-1997;	97US-0048771.
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.	
XX		
PI	Abell LM, Allen SM, Falco SC, Hiltz WD, Kinney AJ;	
PI	Rafalski JA, Thorpe CJ;	
XX		
DR	WPI: 1999-070263/06.	
XX	P-PSDB: AAW97743.	
PT	New plant amino acid biosynthetic enzymes, DNA and chimeric genes -	
PT	encode: dihydrodipicolinate reductase; diaminopimelate epimerase;	
PT	threonine synthase; threonine deaminase; S-adenosylmethionine	
PT	synthetase	
XX		
PS	Claim 44; Page 66-67; 98pp; English.	
XX		
CC	This is the nucleotide sequence of cDNA clone s2.12b06, which	
CC	codes for a full-length soybean S-adenosylmethionine synthetase	
CC	(see AAW97743). The clone was isolated from a soybean seed cDNA	
CC	library and identified by comparison to public sequence databases	
CC	using BLAST algorithms. It shows sequence similarity to the	
CC	tomato enzyme. The invention relates to new isolated nucleic	
CC	acid fragments (see AAX07168-85) encoding plant enzymes (see	
CC	AAW97727-44) that catalyze steps in the biosynthesis of lysine,	
CC	threonine, methionine, cysteine and isoleucine from aspartate, the	
CC	enzyme being selected from dihydrodipicolinate reductase,	
CC	diaminopimelate epimerase, threonine synthase, threonine deamase	
CC	or S-adenosylmethionine synthetase. The invention also relates to	
CC	the construction of a chimeric gene encoding all or a portion of	
CC	the biosynthetic pathway enzyme, in sense or antisense orientation,	
CC	where expression of the chimeric gene results in production of	
CC	altered levels of the enzyme in a transformed host cell.	
CC	Overexpression or reduction of expression of genes encoding the	
CC	amino acid biosynthetic pathway enzymes in crop plants such as	
CC	corn, soybean and wheat can be used to alter levels of the amino	
CC	acids in human food and animal feed. Transformed host cells can	
CC	also be used to identify compounds that inhibit one of the enzymes.	
XX		
XX	Sequence 1485 BP; 366 A; 373 C; 357 G; 389 T; 0 other;	
SQ		
Query Match	22.6%;	Score 53; DB 20; Length 1485;
Best Local Similarity	80.5%;	Pred. No. 4.9e-08;
Matches	62; Conservative	0; Mismatches 15; Indels 0; Gaps 0;
QY	159 caggtcattcaagaccgcgcatacgcgacttggccgtgacgacgcgcgattcaacgtg	218
Db	1156 caggtcttctgaagactgctgcatacgcgacttgcgcagagagagaccctgacttcaatg	1215
QY	219 cgaggtgtcaagcccc	235
Db	1216 ggaagtgtcaagcccc	1232
RESULT	9	
ID	AAAS1037	
XX	AAAS1037 standard; cDNA; 1518 BP.	
XX	AAAS1037;	



XX 21-MAY-1999 (first entry)  
XX  
DE Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.  
XX  
XX S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;  
KW threonine; methionine; cysteine; isoleucine; transgenic plant;  
KW crop improvement; food; feedstuff; ss.  
XX  
OS Zea mays.  
XX  
FH Key Location/Qualifiers  
FT CDS 140..1330  
FT /tag- a  
XX  
XX MO9855601.A2.  
XX  
PD 10-DEC-1998.  
XX  
XX 05-JUN-1998; 98MO-US11692.  
XX  
XX 12-JUN-1997; 97US-0049443.  
PR 06-JUN-1997; 97US-0048771.  
XX  
XX (DUP0 ) DU PONT DE NEMOURS & CO E. I.  
XX  
XX Abell LM, Allen SM, Falco SC, Hiltz WD, Kinney AJ;  
PI Rafalski JA, Thorpe CJ;  
XX  
XX WPI; 1999-070263/06.  
DR P-PSDB; AAW97742.  
XX  
XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -  
PT encode: dihydrotropicolinate reductase; diaminopimelate epimerase;  
PT threonine synthase; threonine deaminase; S-adenosylmethionine  
PT synthetase  
XX  
XX Claim 41; Page 62-63; 98pp; English.  
XX  
XX This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which  
CC codes for a full-length corn S-adenosylmethionine synthetase  
CC (see AAW97742). The clone was isolated from a corn callus cDNA  
CC library and identified by comparison to public sequence databases  
CC using BLAST algorithms. It shows sequence similarity to the  
CC Oryza sativa enzyme. The invention relates to new isolated  
CC nucleic acid fragments (see AAX07168-85) encoding plant enzymes (see  
CC AAW97727-44) that catalyze steps in the biosynthesis of lysine, the  
CC threonine, methionine, cysteine and isoleucine from aspartate, the  
CC enzyme being selected for dihydrotropicolinate reductase,  
CC diaminopimelate epimerase, threonine synthase, threonine deaminase  
CC or S-adenosylmethionine synthetase. The invention also relates to  
CC the construction of a chimeric gene encoding all or a portion of  
CC the biosynthetic pathway enzyme. In sense or antisense orientation,  
CC where expression of the chimeric gene results in production of  
CC altered levels of the enzyme in a transformed host cell.  
CC Overexpression or reduction of expression of genes encoding the  
CC amino acid biosynthetic pathway enzymes in crop plants such as  
CC corn, soybean and wheat can be used to alter levels of the amino  
CC acids in human food and animal feed. Transformed host cells can  
CC also be used to identify compounds that inhibit one of the enzymes.  
XX  
XX Sequence 1582 BP; 340 A; 474 C; 417 G; 351 T; 0 other;

Query Match 21.7%; Score 51; DB 20; Length 1582;  
Best Local Similarity 80.0%; Pred. NO. 2.5e-07;  
Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 161 gttcatcaagacgcgcgaacttgccgtgacgcgcgcgaattcaccctgcg 220  
DB 1230 gctaaccaagacgcgcgaacttgccgtgacgcgcgcgaattcaccctgcg 1289  
OY 221 agtgtgtcaagccccc 235

Db 1290 agtgtgtcaagccccc 1304  
|||||  
RESULT 11  
AAC44219  
ID AAC44219 standard; DNA: 635 BP.  
XX  
XX AAC44219;  
AC  
XX 18-OCT-2000 (first entry)  
DT  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 42062.  
DE  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
XX Arabidopsis thaliana.  
OS  
XX EP1033405-A2.  
PN  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139859.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
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KW metabolic pathway; promoter; termination sequence; ss.  
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
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XX
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
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XX 25-FEB-2000; 2000EP-0301439.
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KM	metabolic pathway; promoter; termination sequence; ss.
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KW protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
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PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query March 21.2%; Score 49.8; DB 21; Length 1654;
Best Local Similarity 77.9%; Pred. No. 6.5e-07;
Matches 60; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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QY 159 caggttcacgaacgcgcatacgcgacttggccgtgacgaagcgcgacttcaactg 218
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QY 219 cgaagtgtgtaagccccc 235
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Db 1288 ggaagtgttcaagccgc 1304
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RESULT 17
AAD02296
ID AAD02296 standard; DNA: 1636 BP.
XX
AC AAD02296;
XX
DT 28-MAR-2001 (first entry)
DE Nicotiana tabacum S-adenosylmethionine synthetase (SAMS) DNA.
XX
KW Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
KM herbicide resistance; S-adenosylmethionine synthetase; SAMS; ds.
XX
OS Nicotiana tabacum.
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XX Key Location/Qualifiers
FH CDS 96..1268
FT /*tag= a
FT /product= "Nicotiana tabacum S-adenosylmethionine
FT synthetase (SAMS) protein"
PN WO200067558-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000MO-US12450.
XX
PR 06-MAY-1999; 99US-0132919.
XX
PA (TIMK/) TIMKO M.
XX
PI Timko M;
XX
DR WPT, 2001-007279/01.
XX
DR P-PSDB; AAV72078.
XX
PT New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
PT e.g. for producing transgenic plants with altered nicotine content.
XX
PS Claim 1: Page 78-79; 103pp; English.
XX
CC The invention relates to enzymes involved in alkaloid, specifically
CC nicotine, synthesis in tobacco and nucleic acids encoding them. The
CC nucleic acid of the invention can be used, in sense or antisense
CC orientation, to produce transgenic tobacco plants with altered
CC alkaloid content, and also for expression of exogenous proteins,
CC e.g. pharmaceutical proteins or proteins implicated in resistance
CC to herbicides. The protein of the invention can be used to
CC identify modulators of enzymatic activity in plants.
CC The present sequence is Nicotiana tabacum S-adenosylmethionine
CC synthetase (SAMS) DNA. This enzyme is involved in the nicotine
CC biosynthetic pathway.
XX
SQ Sequence 1636 BP; 444 A; 365 C; 373 G; 454 T; 0 other;
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Query Match 19.8%; Score 46.6; DB 22; Length 1636;
Best Local Similarity 75.3%; Pred. No. 8.2e-06;
Matches 58; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 219 cgaagtgtgtaagccccc 235
      ||| ||||| ||||| ||
Db 1235 ggaagtgttcaagttcc 1251
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RESULT 18
AAC46421
ID AAC46421 standard; DNA: 1393 BP.
XX
AC AAC46421;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 50076.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX
PN EP1033405-A2.
XX
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PR	23-SEP-1999;	9905-0155486.
PR	24-SEP-1999;	9905-0155659.
PR	28-SEP-1999;	9905-0156458.
PR	29-SEP-1999;	9905-0156596.
PR	04-OCT-1999;	9905-0157117.
PR	05-OCT-1999;	9905-0157753.
PR	06-OCT-1999;	9905-0157865.
PR	07-OCT-1999;	9905-0158029.
PR	08-OCT-1999;	9905-0158232.
PR	12-OCT-1999;	9905-0158369.
PR	13-OCT-1999;	9905-0159293.
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PR	14-OCT-1999;	9905-0159329.
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PR	14-OCT-1999;	9905-0159637.
PR	14-OCT-1999;	9905-0159638.
PR	18-OCT-1999;	9905-0159584.
PR	21-OCT-1999;	9905-0160741.
PR	21-OCT-1999;	9905-0160767.
PR	21-OCT-1999;	9905-0160768.
PR	21-OCT-1999;	9905-0160770.
PR	21-OCT-1999;	9905-0160814.
PR	21-OCT-1999;	9905-0160815.
PR	22-OCT-1999;	9905-0160980.
PR	22-OCT-1999;	9905-0160981.
PR	22-OCT-1999;	9905-0160989.
PR	25-OCT-1999;	9905-0161404.
PR	25-OCT-1999;	9905-0161405.
PR	25-OCT-1999;	9905-0161406.
PR	26-OCT-1999;	9905-0161359.
PR	26-OCT-1999;	9905-0161360.
PR	28-OCT-1999;	9905-0161361.
PR	28-OCT-1999;	9905-0161920.
PR	28-OCT-1999;	9905-0161992.
PR	28-OCT-1999;	9905-0161993.
PR	29-OCT-1999;	9905-0162142.

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Query Match          18.0%; Score 42.4; DB 21; Length 1393;
Best Local Similarity 72.4%; Pred. No. 0.00021;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 160 aggtcatcaagaccgcgcgcatacggccacttggccgtgacgaagccgacttaactgc 219
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Db 1175 aggttcagaaaacgacgcacgctatgtgacattctcgaaagacgaccctgacttaactgc 1234
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OY 220 gaggtggtcaagcccc 235
      |||||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1235 gagtcgtgaagccac 1250

RESULT 19
AAC33674
ID AAC33674 standard; DNA; 1395 BP.
XX
XX AAC33674;
AC
XX
DT 17-OCT-2000 (first entry)
DE
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
PN
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF

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XX	25-FEB-1999	99US-0121825
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PR 12-OCT-1999; 99US-0158369.
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PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159638.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 18.0%; Score 42.4; DB 21; Length 1395;
Beat Local Similarity 72.4%; Pred. No. 0.00021;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Oy 220 gaggtggtcaagccccc 235
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Db 1235 gaggtcgtcaagccac 1250

RESULT 20
AAQ64204
ID AAQ64204 standard; cDNA: 1208 BP.
XX
AC AAQ64204;
XX
DT 18-NOV-1994 (first entry)
XX
DE snac gene encoding enzyme in streptogramin biosynthetic pathway.
XX
KW Antibiotic; streptogramin; snac; snac; snac; biosynthesis; enzyme;
KW biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
OS Streptomyces pristinaespiralis.
XX
FH Key
FT CDS 1..1209 Location/Qualifiers
FT FT /*tag= a
XX
PD FR2696189-A.
XX 01-APR-1994.
XX 25-SEP-1992; 92FR-0011441.
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Pt	Blanc V, Blanche F, Crouzet J, Jacques N, Lacroix P;
Pt	Thibaut D, Zagorec M,
Dx	WPI; 1994-128286/16.
Pt	DNA involved in streptogramin antibiotic biosynthesis - for
Pt	prodn. or bio-conversion of streptogramin(s) or prodn. of
Xx	streptogramin intermediates, derivs. or hybrid antibiotics
Ps	Disclosure; Page 44-47; 83pp; French.
Cc	This sequence comprises the snaA, snab and snac genes which are
Cc	involved in the biosynthesis of streptogramins, antibiotics active
Cc	against Gram-positive bacteria. The identification of the sequences
Cc	encoding the enzymes involved in the biosynthetic pathway means that
Cc	they can be isolated and manipulated. Mutant microorganisms in
Cc	which a step in the streptogramin biosynthetic pathway is blocked
Cc	can be cultured to produce streptogramin intermediates, which may
Cc	later be converted to streptogramin derivatives. Recombinant cells
Cc	may also be used for the bioconversion of streptogramins from one
Cc	form to another or for the production of hybrid antibiotics.
SQ	Sequence 5392 BP; 811 A; 2161 C; 1671 G; 749 T; 0 other;
Query Match	17.1%; Score 40.2; DB 15; Length 5392;
Best Local Similarity	46.7%; Pred. No. 0.0022;
Matches 57; Conservative	0; Mismatches 65; Indels 0; Gaps 0;
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QY	173 ccgcgcgatcacggccacttgcgctgcgcagccgcgacttacctgcgagtggtcaacg 232   Db 4672 ccgcgcgatcacggccacttgcgcgccgactgcgcgacttacctggagcgcgcgacc 4731
QY	233 cc 234   Db 4732 gc 4733
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ID	AAD22684 standard; DNA; 4848 BP.
XX	
AC	AAD22684;
XX	
DT	26-FEB-2002 (first entry)
XX	
DE	Streptomycetes fradiae S-adenosylmethionine (SAM) operon DNA.
XX	
KM	S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KM	MT; methylene tetrahydrofolate reductase; MTHR; activated methyl cycle;
XX	tylosin production; ds.
XX	
OS	Streptomycetes fradiae.
XX	
FH	Key Location/Qualifiers
FT	CDS 986..2209
FT	/tag= a
FT	/product= "SAM synthetase protein"
FT	2241..3341
FT	/tag= b
FT	/product= "methyltransferase protein"
FT	/transl_except= (2241..2243, aa:Met)
FT	3338..4255
FT	/tag= c
FT	/product= "methylene tetrahydrofolate reductase protein"
FT	/transl_except= (3338..3340, aa:Met)
XX	
NN	US6312920-B1.

[illegible]

Pt		Dehoff BS,	Rostock PR;
Xx			
Dn		WPI; 2002-024904/03.	
Pt		New S-adenosylmethionine (SAM) operon from Streptomyces fradiae which	
Xx		tetrahydrofolate reductase, useful for producing SAM by recombinant	
Pt		techniques -	
Xx			
Pt		Claim 19; Column 31-36; 22pp; English.	
Xx			
Cc		The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)	
Cc		operon which comprises three genes encoding SAM synthetase, methyl-	
Cc		transferase (MT), and methylene tetrahydrofolate reductase (MTHR).	
Cc		SAM synthetase, MT and MTHR together comprise the activated methyl	
Cc		cycle which produces SAM and provides methyl groups required for	
Cc		the final steps in tylosin production. The invention also relates	
Cc		to vectors and transformed heterologous host cells for expressing	
Cc		SAM synthetase. It also relates to a method useful for producing	
Cc		SAM by recombinant techniques. The present mRNA sequence is SAM	
Cc		operon from Streptomyces fradiae.	
Xx			
Sq		Sequence 4848 BP; 648 A; 1669 C; 1696 G; 635 U; 0 other:	
Qy		Query Match	17.0%; Score 40; DB 24; Length 4848;
		Best Local Similarity	40.4%; Pred. No. 0.0025;
Matches	44;	Conservative	8; Mismatches 57; Indels 0; Gaps
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Oy		2055 accuccgccgcggcgcaucaucgggaugaccugccgcgcgaucacgcgcaga	2114
Db		173 ccgcgcgataggcacacttgccgtgacagccgaccttacctgcga	221
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		2115 cgcgcgcguacggcccacucugccgcgcgaacucccgagauacucggga	2163
RESULT	24		
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ID	AAA75637 standard; DNA; 1693 BP.		
Xx	AAA75637:		
Dn			
Xx	22-JAN-2001 (first entry)		
DE	Nucleotide sequence of ORF15 encoding S-adenosylmethionine synthetase.		
Kw	Narbanolide synthase; polyketide synthase gene; narbanolide polyketide		
Km	antibiotic; ClI-hydroxyalase; plck; desosamine biosynthesis;		
Kw	desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;		
Km	plicromycin biosynthesis; ss.		
Xx			
OS	Streptomycetes venezuelae.		
Xx			
PN	US6117659-A.		
Xx			
PD	12-SEP-2000.		
Xx			
PF	27-MAY-1999;	99US-0320878.	
Xx			
XX	28-MAY-1998;	98US-0087080.	
PR	22-SEP-1998;	98US-0100880.	
PR	08-FEB-1999;	99US-0119139.	
PR	20-MAY-1999;	99US-0134990.	
PR	30-APR-1997;	97US-0846247.	
PR	06-MAY-1998;	98US-0073538.	
PR	28-AUG-1998;	98US-0141908.	
Xx			
PA	(KOSA-) KOSAN BIOSCIENCES INC.		
Xx			
Xi	Ashley G, Betlach MC, Betlach M, Tang L, McDaniel R.		
Xx			

**P**R 28-AUG-1998; 98US-0141908.  
**P**R 22-SEP-1998; 98US-0100880.  
**PR** 08-FEB-1999; 99US-0119139.

**XX**

(KOSA-) KOSAN BIOSCIENCES INC.

**PA** Ashley G., Betlach MC, Betlach M, McDaniel R, Tang L;  
**PI**  
**XX**

**DR** MPI: 2000-072618/06.  
**PT** P-PsDB: AAY67216, AAY67217.  
**XX**

New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -  
**PS** Disclosure; Page 38; 98pp: English.

This is contig 004 from the recombinant cosmid PKO5023-27 DNA sequence (see AAZ56001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to recombinant DNA containing a coding sequence for a narbonolide PKS. Polyketides are compounds synthesized from 2-carbon units through a series of condensations and subsequent modifications. Modular PKSs are responsible for the production of many antibiotics including plicomycin. The narbonolide PKS consists of a loading module, six extender modules, and two thioester domains. Four proteins make up the narbonolide PKS (*PlcAI*, *PlcAII*, *PlcAIII* and *PlcAIV*). *PlcAI* includes the loading module and extender modules 1 and 2, *PlcAII* includes extender modules 3 and 4, *PlcAIII* includes extender module 5 and *PlcAIV* includes extender module 6 and a type II thioesterase domain. The second type II thioesterase domain is found on the PlCB protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant cosmid PKO5023-27. Narbonolide is desosamylated in S. venezuelae to yield narrowmycin, the desosamine biosynthetic enzyme is required for this conversion, and the desosamine biosynthetic genes are also found in cosmid PKO5023-27. The recombinant DNA of the invention is used to express, in transformed cells, narbonolide (or its derivatives) or other ketolides (particularly hybrids), which may then be converted (e.g. by other enzymes recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human or veterinary medicine.

**SQ** Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;

**OY** Query Match 16.8%; Score 39.4; DB 21; Length 1693;  
Best Local Similarity 47.3%; Pred. No. 0.0025;  
Matches 52; Conservative 0; Mismatches 58; Indels 0; Gaps 0

**Dy** 113 agctacgtttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncaggttcataaga 172  
||||| |

**Dz** 848 ACCTCGGCGGGCCGCATCATCGCGACTTCGTCCGCCGATCTACTCOCAGA 789  
||| |||

**Dy** 173 cgcgcgcatcacggccacttgcgctgaagcaggcgnactaccatgcag 222  
||||| | ||||| ||||| ||||| || || ||||| ||||| |||||

**Dz** 788 CGCGCGCTACGGCCACTTCCGCGCCGAGACTCTCACCTTGAGG 739  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

**RESULT** 26  
**AAB1476**  
**ID ID** AAA81476 standard; DNA: 56485 BP.  
**XX**

**AAA81476:**  
**XX**

**DT DT** 04-DEC-2000 (first entry)  
**DE DE** N. meningitidis partial DNA sequence gmm\_24 SEQ ID NO:24.  
**XX XX**

**KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.**  
**XX XX**

**Neisseria meningitidis**











Query Match 13.0%; Score 30.6; DB 23; Length 606;  
Best Local Similarity 68.9%; Pred. No. 1.7;  
Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 174 cgccgcatacgagcacttgccgtgaacgacgcacacttaccctgcgaagytgcacaagc 233  
|||||  
Db 106 CGCCGCAATACCGCGCTTTCGCCCTTGCCCCGGCGGCATCGCACAAGCGCATGGCCAAAGC 47

OY 234 c 234  
|  
Db 46 C 46

RESULT 35  
AAF12426 AAF12426 standard; cDNA; 657 BP.  
XX  
AC AAF12426;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Aspergillus oryzae EST SEQ ID NO:4949.  
XX  
KW Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; Identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.  
OS Aspergillus oryzae.  
XX  
FN W0200056762-A2.  
PN  
PD 28-SEP-2000.  
XX  
PE 22-MAR-2000; 2000WO-US07781.  
XX  
PR 22-MAR-1999; 99US-0273623.  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
DR WP1: 2000-594572/56.

Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -

Claim 88; Page 2084; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate



DR P-PSDB: AAW81635-36.  
XX  
PT New isolated lepidoptera GABA-gated chloride channels - comprise 3  
PT isoforms isolated from the tobacco budworm *Heliothis virescens*, used  
PT for characterizing bioactive agents, e.g. insecticides  
XX  
PS Claim 1d: Fig 2; 55pp; English.  
XX  
CC This cDNA sequence encompasses the open reading frame encoding  
CC GABA-gated chloride channel TBW-a3 (see AAW81635-36) of tobacco  
CC budworm (*Heliothis virescens*). TBW-a3, TBW-a2 (see AAW81633-34)  
CC and TBW-a1 (see AAW81637) proteins are 3 receptor isoforms that show  
CC sequence homology to each other and to other insect GABA-gated  
CC chloride channels. TBW-2a cDNA was obtained from *H. virescens* 4th  
CC instar larva RNA by PCR and RACE amplifications. The invention  
CC provides expression vectors in which a nucleic acid encoding a  
CC GABA-gated chloride channel is driven by an inducible promoter, and  
CC a claimed process for producing a GABA-gated chloride channel by  
CC transformed cells. The GABA-gated channels or cells expressing  
CC them can be used for characterizing a bioactive agent (claimed),  
CC e.g. for use as an insecticide. Probes and primers that identify  
CC or amplify GABA-gated chloride channel nucleic acids of the  
CC invention are also claimed.  
XX  
SQ Sequence 1519 BP; 421 A; 362 C; 347 G; 388 T; 1 other;  
  
Query Match 12.7%; Score 29.8; DB 20; Length 1519;  
Best Local Similarity 40.5%; Pred. No. 4.8;  
Matches 64; Conservative 0; Mismatches 94; Indels 0; Gaps 0;  
  
QY 2 ttcttcgctacgctcggtgacagatcgacgctgcccattgctgataatgagcgtcct 61  
DB 253 ttcttcctcagacaatttgacgctgctcctcgatgacatacaaaaaagaccggaatt 312  
QY 62 gatccattgctcgctgttataatgtttatataatgagcagacacacgtaagtt 121  
DB 313 gaacttatactgtggtgcagaattcataagaacataatggtaccgacacgctctt 372  
QY 122 nnn 159  
DB 373 gtaaatgaaaagaacatttattccatataagcaaac 410  
  
RESULT 38  
ABL09035  
ID ABL09035 standard; cDNA: 3550 BP.  
XX  
AC ABL09035;  
XX  
DT 26-MAR-2002 (first entry)  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21587.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PE 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
XX  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI: 2001-656860/75.

DR P-PSDB: ABB64932.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Claim 1; SEQ ID NO 21587; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcr\_sequences.  
XX  
SQ Sequence 3550 BP; 1070 A; 899 C; 798 G; 783 T; 0 other;  
  
Query Match 12.6%; Score 29.6; DB 23; Length 3550;  
Best Local Similarity 40.7%; Pred. No. 8.2;  
Matches 59; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
  
QY 82 attaatgttgaattatgacagcagacacacgtaagctnnnnnnnnnnnnnnnnnnnnnn 141  
DB 2107 ataggctgaactcttgacatgagatgacgagacatccatcattgagaccgtgac 2166  
QY 142 nnn 201  
DB 2167 tacttcagcattaagaatcagcttgcagaagctgtggagcagactacaagaagcagat 2226  
QY 202 gacgcagactcactcactgcaggtgg 226  
DB 2227 atcatggtcgtgccctgtgctgtg 2251  
  
RESULT 39  
AAT86246/C  
ID AAT86246 standard; cDNA to mRNA; 1683 BP.  
XX  
AC AAT86246;  
XX  
DT 07-JAN-1998 (first entry)  
DE cDNA encoding mugwort pollen co-factor-independent phosphoglycerate  
DE mutase isoform At11.  
XX  
KW Cofactor-independent phosphoglycerate mutase; PGM-1; E.C. 5.4.21;  
KW Mugwort; pollen; allergy; plant allergen; panallergen; B cell;  
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;  
KW conserved; ds.  
XX  
OS Artemisia vulgaris.  
XX  
FH Key  
FT 1.1683  
FT CDS  
FT /\*tag= a  
XX  
PN WO9705258-A2.  
XX  
PD 13-FEB-1997.  
XX  
PE 02-AUG-1996; 96WO-AT00141.  
XX  
PR 02-AUG-1995; 95AT-0001320.  
XX  
PA (BIOM-) BIOMAT PRODN & HANDELS GMBH.  
XX  
PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;  
XX





XX 22-JUN-2000.  
PD 15-DEC-1999; 99WO-US29823.  
XX 16-DEC-1998; 98US-0112541.  
XX (DUP0 ) DU PONT DE NEMOURS & CO E I.  
XX Famodu OO, Miao G, Sakai H, Lee J, Rafalski JA, Klein TM.  
PI WPI: 2000-431599/37.  
DR P-PSDB: AAY9821.  
XX Polynucleotides encoding plant protein phosphatase useful for  
PT modulating reversible protein phosphorylation in plants -  
XX Claim 4; Page 59; 73pp; English.  
XX The present sequence encodes wheat protein phosphatase 2A regulatory  
CC subunit A. The sequence was identified in clone wrl.pk030.b10:fls of a  
CC cDNA library made from the root of a seven-day-old wheat seedling.  
CC BLAST analysis showed that the present sequence encodes protein  
CC phosphatase 2A regulatory subunit A. The sequence may be used  
CC for the recombinant production of the protein in vivo, e.g. via a gene  
CC therapy protocol, or in vitro, e.g. in fermentation culture. The protein  
CC may then be used to modulate the process of reversible protein  
CC phosphorylation in plants. It may be used directly to supplement a  
CC plant's own production of the enzyme or to rectify mutations that result  
CC in the expression of inactive protein. The protein may also be used to  
CC test for modulators of protein phosphorylation which may be used to  
CC alter the activity of the enzyme.  
XX Sequence 2604 BP; 779 A; 515 C; 579 G; 731 T; 0 other;  
SO

Query Match 12.4%; Score 29.2; DB 21; Length 2604;  
Best Local Similarity 75.8%; Pred. No. 9.8;  
Matches 50; Conservative 0; Mismatches 13; Indels 3; Gaps 1;  
OY 38 ccatgctgataaagcagcgtccatgcatgttcgtgtgttataatgtgtataat 97  
DB 2330 ccatgctgataaagcagcgtccatgcatgttcgtgtgttataatgtgtataat 2386  
OY 98 tgagca 103  
DB 2387 tgagca 2392

RESULT 42  
ABLO4431/C  
ID ABLO4431 standard; cDNA; 1086 BP.  
XX  
XX ABLO4431;  
XX  
XX 26-MAR-2002 (first entry)  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 7775.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7775.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
XX Drosophila melanogaster.  
OS  
XX  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US09231.  
PF 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
XX

PA (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI WPI: 2001-656860/75.  
XX  
XX P-PSDB: ABB60328.  
DR  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PI interactions -  
XX  
XX Claim 1; SEQ ID NO 7775; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA  
CC sequences (ABLO1840-ABU16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
XX Sequence 1086 BP; 295 A; 267 C; 273 G; 251 T; 0 other;  
SO

Query Match 12.3%; Score 29; DB 23; Length 1086;  
Best Local Similarity 40.0%; Pred. No. 7.9;  
Matches 68; Conservative 0; Mismatches 102; Indels 0; Gaps 0;  
OY 36 gcccatgctgataaagcagcgtccatgcatgttcgtgtgttataatgtgtata 95  
DB 943 GCCCATATCCGTACTGAGAGGTCCTCCGTAAGACGTTATTCGGCTAGGTAATAA 884  
OY 96 atgagcagagacaacaacgtaagctttnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 155  
DB 883 ATTGATATGACGACCCCTCCGACGCAAGCATCAGCGGGCTACCGGATCTCCACGTCGG 824  
OY 156 nnnnaggtatcaagaagcgcgcgcatagcgcaccttggccgtyaagcag 205  
DB 823 TGTGCGTGCATCCATCCATGCGACATATCTGTGATGTCCTTATTCGACG 774

RESULT 43  
AAH66738  
ID AAH66738 standard; DNA; 1221 BP.  
XX  
XX AAH66738;  
XX  
XX 26-SEP-2001 (first entry)  
XX C glutamicum coding sequence fragment SEQ ID NO: 1773.  
DE  
XX  
XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
KW organic acid synthesis; ds.  
XX  
XX Corynebacterium glutamicum.  
OS  
XX  
XX EP1108790-A2.  
XX  
XX 20-JUN-2001.  
XX  
XX 18-DEC-2000; 2000EP-0127688.  
XX  
XX 16-DEC-1999; 99JP-0377484.  
PR 07-APR-2000; 2000JP-0159162.  
PR 03-AUG-2000; 2000JP-0280988.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA  
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI

CC The present invention provides a number of nucleotide and protein  
CC sequences from the Corynebacterium bacterium *Corynebacterium glutamicum*. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of *Corynebacterium bacterium*, measuring expression amount and  
CC analysing the expression profile or expression pattern of a gene derived  
CC from *Corynebacterium bacterium*, and identifying a homologue of a gene derived  
CC from *Corynebacterium bacterium*. *Corynebacterium bacterium* are useful for producing  
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a nucleic acid described  
CC in the exemplification of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC European Patent Office.  
XX  
50 Sequence 1221 BP; 272 A; 350 C; 336 G; 263 T; 0 other;

[illegible]

AC AAT04566;  
XX  
XX  
DT 26-APR-1996 (first entry)  
XX  
DE S-adenosylmethionine synthetase DNA.  
XX  
KW S-adenosylmethionine synthetase;  
XX Coryneform bacteria; S-adenosylmethionine synthetase; production; ss  
XX Brevibacterium flavum strain M<sup>C</sup>-233.  
XX

PA (MITU ) MITSUBISHI CHEM CORP  
XX  
DR WPI, 1995-331524/43.  
DR P-PSDB, AAR80060.

CC The DNA encodes a S-adenosylmethionine synthetase derived from a  
CC Corynebacterium bacterium. The DNA is used to transform bacteria to  
CC efficiently produce the enzyme. A 5.5 kb Sail DNA fragment cont.  
CC this DNA gives fragments of 2.4, 1.7 and 1.4 kb when cleaved with  
CC BamHI and fragments of 3.3, 1.0, 0.7 and 0.5 kb when cleaved with PstI  
XX  
XX Sequence 1239 BP; 279 A; 347 C; 339 G; 274 T; 0 other:

[illegible]

RESULT	45
ID	AAF71873 standard; DNA; 1344 BP
XX	AAF71873;
AC	
XX	
DT	30-APR-2001 (first entry)

DE	Corynebacterium glutamicum	MP protein nucleotide sequence	SEQ ID NO:241
XX			
KW	Corynebacterium glutamicum; metabolic pathway protein; MP protein;		
KW	fine chemical production; microorganism; organic acid; nucleoside;		
KW	nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;		
KW	lipid; saturated fatty acid; unsaturated fatty acid; dol; vitamin;		
KW	carbohydrate; aromatic compound; cofactor; polypeptide; enzyme; ds.		
XX			
SS	Corynebacterium glutamicum.		

PN WO200100843-A2.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-IB00923.

PR	25-JUN-1999	9905-0141031
PR	01-JUL-1999	9905-1030476
PR	02-JUL-1999	9905-1032101
PR	08-JUL-1999	9905-1031415
PR	08-JUL-1999	9905-1031418
PR	08-JUL-1999	9905-1031419
PR	08-JUL-1999	9905-1031420
PR	08-JUL-1999	9905-1031424
PR	08-JUL-1999	9905-1031428
PR	08-JUL-1999	9905-1031434
PR	08-JUL-1999	9905-1031435
PR	08-JUL-1999	9905-1031443
PR	08-JUL-1999	9905-1031457
PR	08-JUL-1999	9905-1031465
PR	08-JUL-1999	9905-1031478
PR	08-JUL-1999	9905-1031510
PR	08-JUL-1999	9905-1031541





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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 23:47:41 ; Search time 76.72 Seconds  
(without alignments)  
752.397 Million cell updates/sec

Title: US-09-198-779b-1

Perfect score: 235  
Sequence: 1 gtttcgcctagcctcggt.....ctgcgagtggtcgaacccc 235

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/6C.COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40.2	17.1	1208	2	US-08-403-852D-4	Sequence 4, Appl1
2	40.2	17.1	1208	3	US-08-510-646B-4	Sequence 4, Appl1
3	40.2	17.1	1208	4	US-09-231-818-4	Sequence 4, Appl1
4	40.2	17.1	5392	2	US-08-403-852D-1	Sequence 1, Appl1
5	40.2	17.1	5392	3	US-08-510-646B-1	Sequence 1, Appl1
6	40.2	17.1	5392	4	US-09-231-818-1	Sequence 1, Appl1
7	40	17.0	4848	4	US-08-955-957A-1	Sequence 1, Appl1
8	40	17.0	4848	4	US-08-955-957A-4	Sequence 1, Appl1
9	40	17.0	4848	4	US-08-955-957A-6	Sequence 1, Appl1
10	39.4	16.8	1693	3	US-09-320-878-23	Sequence 6, Appl1
11	34.4	14.6	4403765	4	US-09-103-840A-2	Sequence 23, Appl1
12	34.4	14.6	4411529	4	US-09-103-840A-1	Sequence 2, Appl1
13	29.8	12.7	1519	4	US-09-002-361-4	Sequence 1, Appl1
14	29.6	12.6	594	4	US-08-804-372A-31	Sequence 4, Appl1
15	28.8	12.3	767	4	US-08-139-909-1	Sequence 31, Appl1
16	28.8	12.3	767	2	US-08-308-821A-1	Sequence 1, Appl1
17	28.8	12.3	767	3	US-08-831-627-1	Sequence 1, Appl1
18	28.6	12.2	1957	4	US-09-352-890-11	Sequence 11, Appl1
19	28.4	12.1	4560	4	US-09-256-703-1	Sequence 11, Appl1
20	28.4	12.1	5430	3	US-09-012-515A-11	Sequence 11, Appl1
21	28.4	12.1	5430	3	US-08-360-144A-11	Sequence 11, Appl1
22	28.4	12.1	5635	3	US-08-136-742A-3	Sequence 11, Appl1
23	28.4	12.1	5635	5	US-09-248-026-3	Sequence 3, Appl1
24	28.4	12.1	5635	5	PCT-US93-11667-3	Sequence 3, Appl1
25	28.4	12.1	6126	2	US-08-951-912-3	Sequence 3, Appl1
26	28.4	12.1	6126	4	US-09-174-077-3	Sequence 3, Appl1
27	28.4	12.1	6129	1	US-07-637-621-1	Sequence 1, Appl1

C 28	28.4	12.1	6129	1	US-08-136-742A-1	Sequence 1, Appl1
C 29	28.4	12.1	6129	1	US-08-135-809A-1	Sequence 1, Appl1
C 30	28.4	12.1	6129	2	US-08-951-912-1	Sequence 1, Appl1
C 31	28.4	12.1	6129	2	US-08-951-912-5	Sequence 5, Appl1
C 32	28.4	12.1	6129	2	US-08-691-605-1	Sequence 1, Appl1
C 33	28.4	12.1	6129	3	US-09-248-026-1	Sequence 1, Appl1
C 34	28.4	12.1	6129	4	US-08-681-838A-1	Sequence 1, Appl1
C 35	28.4	12.1	6129	4	US-09-174-077-1	Sequence 1, Appl1
C 36	28.4	12.1	6129	4	US-09-174-077-5	Sequence 5, Appl1
C 37	28.4	12.1	6129	5	PCT-US93-11667-1	Sequence 1, Appl1
C 38	28.4	12.1	6130	1	US-08-466-886-16	Sequence 16, Appl1
C 39	28.4	12.1	6130	2	US-08-604-488-1	Sequence 1, Appl1
C 40	28.4	12.1	6130	2	US-08-469-461-1	Sequence 1, Appl1
C 41	28.4	12.1	6130	3	US-07-890-609-1	Sequence 1, Appl1
C 42	28.4	12.1	6130	3	US-08-030-081-1	Sequence 1, Appl1
C 43	28.4	12.1	6130	4	US-08-469-617-16	Sequence 16, Appl1
C 44	28.4	12.1	6146	6	5240846-4	Sequence 1, Appl1
C 45	28.4	12.1	7653	4	US-08-471-112A-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-403-852D-4  
; Sequence 4, Appl1cation US/08403852D  
; Patent No. 5891695  
; GENERAL INFORMATION:  
; APPLICANT: Blanc, Veronique  
; APPLICANT: Blanc, Francis  
; APPLICANT: Crouzet, Joel  
; APPLICANT: Jacques, Nathalie  
; APPLICANT: Lacroix, Patricia  
; APPLICANT: Thibaut, Denis  
; APPLICANT: Zagorec, Monique  
; APPLICANT: Debussche, Laurent  
; APPLICANT: De Crecy-Lagard, Valerie  
; TITLE OF INVENTION: Polypeptides Involved In The  
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences  
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; City: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,852D  
; FILING DATE: 10-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR 93/00923  
; FILING DATE: 25-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 92/11441  
; FILING DATE: 25-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03806, 0054-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1208 base pairs  
; TYPE: nucleic acid

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? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cdna
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: S.pristinaeapitalis
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1208
? OS=08-403-852D-4
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Query Match	17.1%	Score 40.2	DB 2	Length 1208
Best Local Similarity	46.7%	Pred. No. 0.00012		
Matches 57, Conservative	0	Mismatches 65	Indels 0	Gaps 0

[illegible]

RESULT 2  
US-08-510-646B-4

Sequence 4 Application US/08510646B  
Patent No. 6077699

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique  
APPLICANT: Blanche, Francis  
APPLICANT: Crouzet, Joel  
APPLICANT: Jacques, Nathalie  
APPLICANT: Lacroix, Patricia  
APPLICANT: Thibaut, Denis  
APPLICANT: Zagorec, Monique  
APPLICANT: Debussche, Laurent  
APPLICANT: De Crecy-Lagard, Valerie  
TITLE OF INVENTION: Polypeptides Involved In The  
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences  
TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
NUMBER OF SPOUNCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farbow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/510,646B  
FILING DATE: 03-AUG-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/403,852  
FILING DATE: 10-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR 93/00923  
FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441  
FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03806.0054-010000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ. ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1208 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: S.pristinaespiralis  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1208  
 US-08-510-646B-4

Query Match	17.1%;	Score 40.2;	DB 3;	Length 1208;
Best Local Similarity	46.7%;	Pred. No. 0.00012;		
Matches 57;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0

[illegible]

RESULT 3  
 US-09-231-818-4  
 Sequence 4, Application US/09231818  
 Patent No. 6171846  
 GENERAL INFORMATION:  
 APPLICANT: Blanc, Veronique  
 APPLICANT: Blanche, Francis  
 APPLICANT: Crouzet, Joel  
 APPLICANT: Jacques, Nathalie  
 APPLICANT: Lacroix, Patricia  
 APPLICANT: Thibaut, Denis  
 APPLICANT: Zagorec, Monique  
 APPLICANT: Debussche, Laurent  
 APPLICANT: De Creely, Lagard, Valerie  
 TITLE OF INVENTION: Polypeptides Involved In The  
 TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences  
 TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/231,818











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; Patent No. 6329516
;
; GENERAL INFORMATION:
; APPLICANT: Halling, Blaik
; TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
; TITLE OF INVENTION: Channels
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,361
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1443
; OTHER INFORMATION:
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; US-09-002-361-4
;
Query Match          12.7%; Score 29.8; DB 4; Length 1519;
Best Local Similarity 40.5%; Pred. No. 0.59;
Matches 64; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
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DB 253 TTTTACTTACAGACATTTTGGACTGATCTCGATTAGCATACAAAAAGACCGAGATT 312
;
OY 62 gatccatgctgctgctgctatcatatgctgtataatgagcagagacacacgctacgt 121
DB 313 GAAACTTATCTGCTGGGCTCAGCAATCATTAAGAAACATATGGGTACCGACAGCTTCTT 372
;
OY 122 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 159
DB 373 GTAATGAAAAGCAATCTTATTTCATATAGCAACAAC 410
;
;
RESULT 14
US-08-804-372A-31
; Sequence 31, Application US/08804372A
; Patent No. 6183753
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Wild, Martha A.
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
; THEREOF
```

```

; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,372A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2552/39115E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..594
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; US-08-804-372A-31
;
Query Match          12.6%; Score 29.6; DB 4; Length 594;
Best Local Similarity 64.7%; Pred. No. 0.45;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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DB 87 CACCGCCTCCGCTGACGACCACTTCGCCCCGACGAGCCACCTTCTGCGCAGACCT 146
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OY 228 caagcccc 235
DB 147 CCAGCTCC 154
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RESULT 15
US-08-139-909-1
; Sequence 1, Application US/08139909
; Patent No. 5641656
; GENERAL INFORMATION:
; APPLICANT: Sekellick, Margaret J.
; TITLE OF INVENTION: CHICKEN INTERFERON GENE AND NOVEL
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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RESULT 16  
 US-08-308-821A-1  
 : Sequence 1, Application US/08308821A  
 : Patent No. 5885567  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Sekelick, Margaret J.  
 : APPLICANT: Marcus, Philip I.  
 : APPLICANT: Ferrandino, Anthony F.  
 : TITLE OF INVENTION: AVIAN INTERFERON GENES, NOVEL  
 : TITLE OF INVENTION: RECOMBINANT DNA AND PROTEINS  
 : NUMBER OF SEQUENCES: 6  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 : STREET: Two Millitia Drive  
 : CITY: Lexington  
 : STATE: Massachusetts  
 : COUNTRY: USA  
 :  
 : ZIP: 02173  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC Compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/308,821A  
 : FILING DATE: 19-SEP-1994  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/235,402  
 : FILING DATE: 28-APR-1994  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/139,909  
 : FILING DATE: 22-OCT-1993

RESULT 17  
 US-08-831-627-1  
 Sequence 1, Application US/08831627  
 Patent No. 6020465  
 GENERAL INFORMATION:  
 APPLICANT: Sekellick, Margaret J.  
 APPLICANT: Marcus, Philip I.  
 APPLICANT: Ferrandino, Anthony F.  
 TITLE OF INVENTION: CHICKEN INTERFERON GENE AND NOVEL  
 TITLE OF INVENTION: RECOMBINANT DNA  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Millitia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02173  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/831,627  
 FILING DATE: 09-APR-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/235,402  
 FILING DATE: 28-APR-1994  
 APPLICATION NUMBER: US 08/139,909  
 FILING DATE: 22-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carroll, Alice O.  
 REGISTRATION NUMBER: 33,542  
 REFERENCE/DOCKET NUMBER: UCT93-04A  
 TELECOMMUNICATION INFORMATION:



INFORMATION FOR SEQ ID NO: 11;

MOLECULE TYPE: CDNA  
US-08-136-742A-3











RESULT 33  
 : Sequence 1, Application US/09248026  
 : Patent No. 6093567  
 : GENERAL INFORMATION:  
 : APPLICANT: Gregory, R.J., Armentano, D., Couture, L.A., Smith,  
 : A.E.  
 : TITLE OF INVENTION: ADENOVIRUS VECTORS FOR GENE THERAPY  
 : NUMBER OF SEQUENCES: 10  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESSEE: BAKER & BOTTS, L.L.P.  
 : STREET: 30 ROCKEFELLER PLAZA  
 : CITY: NEW YORK  
 : STATE: NEW YORK  
 : COUNTRY: USA  
 : ZIP: 10112  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/248,026  
 : FILING DATE: 10-FEB-1999  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/895,194  
 : FILING DATE: 16-JUL-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Seide, Rochelle K.

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RESULT 34
US-08-681-838A-1/c
: Sequence 1, Application US/08681838A
: Patent No. 6245735
: GENERAL INFORMATION:
: APPLICANT: pier, Gerald B
: TITLE OF INVENTION: Methods and Products for Treating
: TITLE OF INVENTION: Pseudomonas Infection
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: wolf, Greenfield & Sacks PC
: STREET: 600 Atlantic Avenue
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/681,838A
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Gates, Edward R
: REGISTRATION NUMBER: 31,616
: REFERENCE/DOCKET NUMBER: B0801/7054
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6129 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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RESULT 45  
US-08-471-112A-1/c  
; Sequence 1, Application US/08471112A  
; Patent No. 6313264  
GENERAL INFORMATION  
; APPLICANT: Molnar-Kimber, Katherine L.  
; FALLILI, Amedeo F.  
; APPLICANT: Caggiano, Thomas J.





Gencore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 00:26:11 ; Search time 3447.21 Seconds

(without alignments)  
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Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2	198	84.3	235	16 US-09-236-218A-2024	Sequence 2024, Ap
3	198	84.3	235	35 US-09-955-568-2024	Sequence 2024, Ap
4	198	84.3	242	17 US-09-304-517A-936	Sequence 936, App
5	198	84.3	242	17 US-09-371-146A-936	Sequence 936, App
6	198	84.3	242	36 US-09-985-678-936	Sequence 936, App
7	198	84.3	482	25 US-09-654-617-259077	Sequence 259077, App
8	198	84.3	482	27 US-09-684-016-259077	Sequence 259077, App
9	121	51.5	368	33 US-09-865-419A-16999	Sequence 16999, A
10	121	51.5	399	23 US-09-619-643-138	Sequence 138, App
11	121	51.5	399	53 US-60-146-907-8	Sequence 8, Appl
12	121	51.5	449	59 US-60-207-458-58459	Sequence 58459, A
13	121	51.5	503	59 US-60-207-458-58453	Sequence 58453, A
14	121	51.5	503	59 US-60-207-458-15364	Sequence 15364, A
15	121	51.5	509	32 US-09-842-214-9449	Sequence 9449, Ap
16	121	51.5	509	59 US-60-207-214-9449	Sequence 9449, Ap
17	121	51.5	526	33 US-09-873-402A-43368	Sequence 43368, A
18	121	51.5	528	33 US-09-865-419A-52142	Sequence 52142, A
19	121	51.5	547	33 US-09-865-419A-92675	Sequence 92675, A
20	121	51.5	547	59 US-60-207-458-136690	Sequence 136690, A
21	121	51.5	556	33 US-09-865-439A-95421	Sequence 95421, A
22	121	51.5	560	59 US-60-207-458-139436	Sequence 139436, A
23	121	51.5	607	33 US-09-865-439A-62153	Sequence 62153, A
24	121	51.5	607	59 US-60-207-458-106313	Sequence 106313, A
25	121	51.5	615	33 US-09-873-402A-84677	Sequence 84677, A
26	121	51.5	615	59 US-60-209-830-56416	Sequence 56416, A
27	121	51.5	2233	25 US-09-654-617-259066	Sequence 259066, A
28	119.4	50.8	240	23 US-09-684-016-259066	Sequence 259066, A
29	119.4	50.8	267	53 US-09-619-643-15485	Sequence 15485, A
30	117.8	50.1	468	59 US-60-145-485-8575	Sequence 8575, Ap
31	117.8	50.1	468	59 US-60-207-458-55943	Sequence 55943, A

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES







QY 121 t 121  
Db 368 t 368

## RESULT 11

US-60-146-907-8  
Sequence 8, Application US/60146907  
GENERAL INFORMATION:  
APPLICANT: Fisher, Dane K.  
APPLICANT: Lalgudi, Raghunath V.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
FILE REFERENCE: 38-21(51365)A  
CURRENT APPLICATION NUMBER: US/60/146, 907  
CURRENT FILING DATE: 1999-08-02  
NUMBER OF SEQ ID NOS: 3607  
SEQ ID NO 8  
LENGTH: 399  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3115-014-P1-K1-G4  
US-60-146-907-8

Query Match 51.5%; Score 121; DB 53; Length 399;  
Best Local Similarity 100.0%; Pred. No. 6, 8e-29;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgctagcctcggtgacagatcgacgctgcccataatgagcgtcc 60  
|||||  
Db 248 gtttcgctagcctcggtgacagatcgacgctgcccataatgagcgtcc 307  
|||||  
QY 61 tgatccattgctggtgtgtatataatgtgacagacacacacgtacgt 120  
|||||  
Db 308 tgatccattgctggtgtgtatataatgtgacagacacacacgtacgt 367  
|||||  
QY 121 t 121  
Db 368 t 368

## RESULT 12

US-60-207-458-58459/c  
Sequence 58459, Application US/60207458  
GENERAL INFORMATION:

APPLICANT: Abad, Mark S.  
APPLICANT: Conner, Timothy W.  
APPLICANT: Deikman, Jill  
APPLICANT: Hardeman, Kristine J.  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Lalgudi, Raghunath V.  
APPLICANT: Ruan, Yijun G.  
APPLICANT: Ruff, Thomas G.  
APPLICANT: Sammons, R. Douglas  
APPLICANT: Shukla, Hridayabhiranjan  
APPLICANT: Wu, Kunsheng  
APPLICANT: Xu, Nanfei  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
FILE REFERENCE: 38-21(51936)A  
CURRENT APPLICATION NUMBER: US/60/207, 458  
CURRENT FILING DATE: 2000-05-30  
NUMBER OF SEQ ID NOS: 152403  
SEQ ID NO 58459  
LENGTH: 449  
TYPE: DNA  
ORGANISM: Zea mays  
OTHER INFORMATION: Clone ID: uc-zmflb73012c08a2  
US-60-207-458-58459

Query Match 51.5%; Score 121; DB 59; Length 449;  
Best Local Similarity 100.0%; Pred. No. 7, 1e-29;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgctagcctcggtgacagatcgacgctgcccataatgagcgtcc 60  
|||||  
Db 121 gtttcgctagcctcggtgacagatcgacgctgcccataatgagcgtcc 62  
|||||  
QY 61 tgatccattgctggtgtgtatataatgtgacagacacacacgtacgt 120  
|||||  
Db 61 tgatccattgctggtgtgtatataatgtgacagacacacacgtacgt 2  
|||||  
QY 121 t 121  
Db 1 t 1

## RESULT 13

US-60-207-458-58453/c  
Sequence 58453, Application US/60207458  
GENERAL INFORMATION:

APPLICANT: Abad, Mark S.  
APPLICANT: Conner, Timothy W.  
APPLICANT: Deikman, Jill  
APPLICANT: Hardeman, Kristine J.  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Lalgudi, Raghunath V.  
APPLICANT: Ruan, Yijun G.  
APPLICANT: Ruff, Thomas G.  
APPLICANT: Sammons, R. Douglas  
APPLICANT: Shukla, Hridayabhiranjan  
APPLICANT: Wu, Kunsheng  
APPLICANT: Xu, Nanfei  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
FILE REFERENCE: 38-21(51936)A  
CURRENT APPLICATION NUMBER: US/60/207, 458  
CURRENT FILING DATE: 2000-05-30  
NUMBER OF SEQ ID NOS: 152403  
SEQ ID NO 58453  
LENGTH: 473  
TYPE: DNA  
ORGANISM: Zea mays  
OTHER INFORMATION: Clone ID: uc-zmflb73012b12a2  
US-60-207-458-58453

Query Match 51.5%; Score 121; DB 59; Length 473;  
Best Local Similarity 100.0%; Pred. No. 7, 2e-29;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgctagcctcggtgacagatcgacgctgcccataatgagcgtcc 60  
|||||  
Db 127 gtttcgctagcctcggtgacagatcgacgctgcccataatgagcgtcc 68  
|||||  
QY 61 tgatccattgctggtgtgtatataatgtgacagacacacacgtacgt 120  
|||||  
Db 67 tgatccattgctggtgtgtatataatgtgacagacacacacgtacgt 8  
|||||  
QY 121 t 121  
Db 7 t 7

## RESULT 14

US-60-207-458-15364/c  
Sequence 15364, Application US/60207458  
GENERAL INFORMATION:

APPLICANT: Abad, Mark S.  
APPLICANT: Conner, Timothy W.  
APPLICANT: Deikman, Jill  
APPLICANT: Hardeman, Kristine J.

```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ruaf, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 15364
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmf1mo17346c10a1
US-60-207-458-15364
```

```
Query Match
Best Local Similarity 51.5%; Score 121; DB 59; Length 502;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 gtttcgctagcctcggtgacagatcgacgtgcccacgtgataatgagcgtcc 60
Db 146 GTTTCCGCTAGCCTCGGTGACAGATCGACGTCGCCATCTGATAATGACGGTCC 87
Qy 61 tgatccattgttcgtgtgtatataatgttataatgagcagacacagctagct 120
Db 86 TGATCCATTGTTGCTGTGTATTATATGTTATATTGAGACAGACACACGCTAGCT 27
Qy 121 t 121
Db 26 T 26
```

```
RESULT 15
US-09-849-526A-9449/c
; Sequence 9449, Application US/09849526A
; GENERAL INFORMATION:
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Shukla, Hridayabhiranjan
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.250(38-21(51930)B)
; CURRENT APPLICATION NUMBER: US/09/849,526A
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/202,214
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/816,660
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 30131
; SEQ ID NO 9449
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: uc-zmroteosinte073b07a1
US-09-849-526A-9449
```

```
Query Match
Best Local Similarity 51.5%; Score 121; DB 32; Length 509;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Db 133 GTTTCCGCTAGCCTCGGTGACAGATCGACGTCGCCATGCTGATAATGACCGTCC 74
Qy 61 tgatccattgttcgtgtgtatataatgttataatgagcagacacacagctagct 120
Db 73 TGATCCATTGTTGCTGTGTATTATATGTTATATTGATTAATGAGACAGACACGCTAGCT 14
Qy 121 t 121
Db 13 T 13

RESULT 16
US-60-202-214-9449/c
; Sequence 9449, Application US/60202214
; GENERAL INFORMATION:
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Shukla, Hridayabhiranjan
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
; FILE REFERENCE: 38-21(51930)A
; CURRENT APPLICATION NUMBER: US/60/202,214
; CURRENT FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 29880
; SEQ ID NO 9449
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmroteosinte073b07a1
US-60-202-214-9449

Query Match
Best Local Similarity 51.5%; Score 121; DB 59; Length 509;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 gtttcgctagcctcggtgacagatcgacgtgcccacgtgataatgagcgtcc 60
Db 133 GTTTCCGCTAGCCTCGGTGACAGATCGACGTCGCCATGCTGATAATGAGACGGTCC 74
Qy 61 tgatccattgttcgtgtgtatataatgttataatgagcagacacacagctagct 120
Db 73 TGATCCATTGTTGCTGTGTATTATATGTTATATTGATTAATGAGACAGACACGCTAGCT 14
Qy 121 t 121
Db 13 T 13

RESULT 17
US-09-873-402A-43368/c
; Sequence 43368, Application US/09873402A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: Varagona, Marguerite J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51934)B
; CURRENT APPLICATION NUMBER: US/09/873,402A
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,830
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 90966
; SEQ ID NO 43368
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3595-016-Q1-N6-G8
US-09-873-402A-43368
```

```
Query Match          51.5%; Score 121; DB 33; Length 526;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttaagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 121 GTTTCCGCTAGCCCTGCGTGAGACAGATCGACGCTGCCCATGCTGATTAATGAGACGGTCC 62

QY 61 tgatccattgtcgtgtgtatataatgctgtataattgagcagagacacacgctacgt 120
    |||||||
Db 61 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGAGCAGACACACACGTACGT 2

QY 121 t 121
    |
Db 1 T 1

RESULT 18
US-09-865-419A-52142/c
; Sequence 52142, Application US/09865419A
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(51935)B
; CURRENT APPLICATION NUMBER: US/09/865,419A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/208,063
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 54020
; SEQ ID NO 52142
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3637-241-Q6-N6-A4
US-09-865-419A-52142

Query Match          51.5%; Score 121; DB 33; Length 528;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttaagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 127 GTTTCCGCTAGCCCTGCGTGAGACAGATCGACGCTGCCCATGCTGATTAATGAGACGGTCC 68

QY 61 tgatccattgtcgtgtgtatataatgctgtataattgagcagagacacacgctacgt 120
    |||||||
Db 67 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGAGCAGACACACACGTACGT 8

QY 121 t 121
    |
Db 7 T 7

RESULT 19
US-09-865-439A-92675/c
; Sequence 92675, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerman, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 92675
```

```
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3607-012-Q6-N6-H9
US-09-865-439A-92675

Query Match          51.5%; Score 121; DB 33; Length 547;
Best Local Similarity 100.0%; Pred. No. 7.6e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttaagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 127 GTTTCCGCTAGCCCTGCGTGAGACAGATCGACGCTGCCCATGCTGATTAATGAGACGGTCC 68

QY 61 tgatccattgtcgtgtgtatataatgctgtataattgagcagagacacacgctacgt 120
    |||||||
Db 67 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGAGCAGACACACACGTACGT 8

QY 121 t 121
    |
Db 7 T 7

RESULT 20
US-60-207-458-136690/c
; Sequence 136690, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Delkman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laljudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 136690
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3607-012-Q6-N6-H9
US-60-207-458-136690

Query Match          51.5%; Score 121; DB 59; Length 547;
Best Local Similarity 100.0%; Pred. No. 7.6e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttaagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 127 GTTTCCGCTAGCCCTGCGTGAGACAGATCGACGCTGCCCATGCTGATTAATGAGACGGTCC 68

QY 61 tgatccattgtcgtgtgtatataatgctgtataattgagcagagacacacgctacgt 120
    |||||||
Db 67 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGAGCAGACACACACGTACGT 8

QY 121 t 121
    |
Db 7 T 7

RESULT 21
```

```
US-09-865-439A-95421/c
; Sequence 95421, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 95421
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3607-012-Q6-N7-H9
US-09-865-439A-95421
```

```
Query Match
Best Local Similarity 100.0%; Score 121; DB 33; Length 560;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtttcgctcagcctcgggtagacagatcgacgctgcccacgtgataatggaagctcc 60
    |||||||
Db 127 gttttccgctgagcctcgggtagacagatcgacgctgcccacgtgataatggaagctcc 68
    |||||||

Qy 61 tgatccattgctgctgtgtatataatgttataatgagacagacacagctagct 120
    |||||||
Db 67 tgatccattgctgctgtgtgtattatattgttattgagacagacacacagctagct 8
    |||||||

Qy 121 t 121
Db 7 T 7
```

```
RESULT 22
US-60-207-458-139436/c
; Sequence 139436, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Delkman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laljudi, Raghumath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 139436
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3607-012-Q6-N7-H9
US-60-207-458-139436
```

```
Query Match
Best Local Similarity 100.0%; Score 121; DB 59; Length 560;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 gtttcgctcagcctcgggtagacagatcgacgctgcccacgtgataatggaagctcc 60
    |||||||
Db 127 gttttccgctgagcctcgggtagacagatcgacgctgcccacgtgataatggaagctcc 68
    |||||||

Qy 61 tgatccattgctgctgtgtatataatgttataatgagacagacacagctagct 120
    |||||||
Db 67 tgatccattgctgctgtgtgtattatattgttattgagacagacacacagctagct 8
    |||||||

Qy 121 t 121
Db 7 T 7
```

```
RESULT 23
US-09-865-439A-62153/c
; Sequence 62153, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 62153
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3587-218-Q1-N6-F8
US-09-865-439A-62153
```

```
Query Match
Best Local Similarity 100.0%; Score 121; DB 33; Length 607;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtttcgctcagcctcgggtagacagatcgacgctgcccacgtgataatggaagctcc 60
    |||||||
Db 127 gttttccgctgagcctcgggtagacagatcgacgctgcccacgtgataatggaagctcc 68
    |||||||

Qy 61 tgatccattgctgctgtgtatataatgttataatgagacagacacacagctagct 120
    |||||||
Db 67 tgatccattgctgctgtgtgtattatattgttattgagacagacacacagctagct 8
    |||||||

Qy 121 t 121
Db 7 T 7
```

```
RESULT 24
US-60-207-458-106313/c
; Sequence 106313, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Delkman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laljudi, Raghumath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 106313
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3607-012-Q6-N7-H9
US-60-207-458-106313
```

```
Query Match
Best Local Similarity 100.0%; Score 121; DB 59; Length 560;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```





US-09-684-016-259066/C  
; Sequence 259066, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jindong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/684,016  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; NUMBER OF SEQ ID NOS: 2000-09-05  
; SEQ ID NO 259066  
; LENGTH: 2233  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-684-016-259066

Query Match 51.5%; Score 121; DB 27; Length 2233;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtttcgctagcctcggtgacagatcgacgctgcccattgataatgagcgtcc 60  
DB 216 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTCCCATGCTGATTAATGAGCGTCC 157  
OY 61 tgatccattgctcgttggtatattgtgtataattgagcagagacacacgtagt 120  
DB 156 TGATCCATTGCTGTTGTTTATTATTAATTGATTAATGAGCAGACACACGCTAGCT 97  
OY 121 t 121  
DB 96 T 96

RESULT 29  
US-09-619-643-15485/C  
; Sequence 15485, Application US/09619643  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalguadi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(51230)B  
; CURRENT APPLICATION NUMBER: US/09/619,643  
; CURRENT FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 15485  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3150-107-P2-K1-E3  
US-09-619-643-15485

Query Match 50.8%; Score 119.4; DB 23; Length 240;  
Best Local Similarity 99.2%; Pred. No. 1.9e-28;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 gtttcgctagcctcggtgacagatcgacgctgcccattgataatgagcgtcc 60  
DB 121 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTCCCATGCTGATTAATGAGCGTCC 62  
OY 61 tgatccattgctcgttggtatattgtgtataattgagcagagacacacgtagt 120  
DB 61 TGATCCATTGCTGTTGTTTATTATTAATTGATTAATGAGCAGACACACGCTAGCT 2  
OY 121 t 121  
DB 1 T 1

RESULT 30  
US-60-145-485-8575/C  
; Sequence 8575, Application US/60145485  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Deng, Molian  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Miller, Phillip W.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(51229)A  
; CURRENT APPLICATION NUMBER: US/60/145,485  
; CURRENT FILING DATE: 1999-07-23  
; NUMBER OF SEQ ID NOS: 9366  
; SEQ ID NO 8575  
; LENGTH: 267  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3150-107-P2-K1-E3  
US-60-145-485-8575

Query Match 50.8%; Score 119.4; DB 53; Length 267;  
Best Local Similarity 99.2%; Pred. No. 2e-28;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 gtttcgctagcctcggtgacagatcgacgctgcccattgataatgagcgtcc 60  
DB 148 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTCCCATGCTGATTAATGAGCGTCC 89  
OY 61 tgatccattgctcgttggtatattgtgtataattgagcagagacacacgtagt 120  
DB 88 TGATCCATTGCTGTTGTTTATTATTAATTGATTAATGAGCAGACACACGCTAGCT 29  
OY 121 t 121  
DB 28 T 28

RESULT 31  
US-60-207-458-56943/C  
; Sequence 56943, Application US/60207458  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Deikman, Jill  
; APPLICANT: Hardeman, Kristine J.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Lalguadi, Raghunath V.  
; APPLICANT: Ruan, Yijun G.  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Sammons, R. Douglas  
; APPLICANT: Shukla, Hridayabhiranjan  
; APPLICANT: Wu, Kunsheng  
; APPLICANT: Xu, Nanfei  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(51936)A  
; CURRENT APPLICATION NUMBER: US/60/207,458  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 152403  
; SEQ ID NO 56943  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: uc-2mf1b73347d11a1  
US-60-207-458-56943

Query Match 50.1%; Score 117.8; DB 59; Length 468;  
Best Local Similarity 98.3%; Pred. No. 8.1e-28;  
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 32
US-09-873-402A-85870/C
Sequence 85870, Application US/09873402A
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
APPLICANT: Varasgona, Marguerite J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51934)B
CURRENT APPLICATION NUMBER: US/09/873,402A
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,830
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 90966
SEQ ID NO 85870
LENGTH: 609
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3689-238-01-N6-G5
US-09-873-402A-85870

```

```

RESULT 34
US-09-865-439A-71349/C
Sequence 71349, Application US/09865439A
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(51936)B
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 71349
LENGTH: 713
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: jC-zmsHLIB3587P001h03a1
US-09-865-439A-71349

```

```

Query March 48.1%; Score 113; DB 33; Length 713;
Best Local Similarity 95.9%; Pred. No. 3.5e-26;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 gtttcgcgtacgctcggctgagacagatcgacgctgcccatgctgataaatgagcggtc 60
          |||
Db       131 GTTTCCTCCTTACGAGCTCGGTGACAGATCGACGCTGCCAATGATGAGACGGCTCC 72
          |||

QY      61 tgatccattgctcgcttggtattcaatgctgtatcaattgagcagagacaacagctact 120
          |||
Db       71 TGATCCATTGCTTCGTTGTTGTTATTATGTTGTATTAATTGAGCAGGACTCTACACAAACA 12
          |||

QY      121 t
          |
Db       11 T 11

RESULT 35
US-60-207-458-115496/c
; Sequence 115496, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laligudi, Ragunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayahiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
; TITLE OF INVENTION: PLANTS

```

```
FILE REFERENCE: 38-21(51936)A
CURRENT APPLICATION NUMBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 152403
SEQ ID NO 115496
LENGTH: 713
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: jC-zmshLIB3587P001h03a1
US-60-207-458-115496
```

```
Query Match
Best Local Similarity 48.1%; Score 113; DB 59; Length 713;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgccatgctgtataatgagcgctcc 60
Db 131 GTTTCCGCTAGCCCTCGGTGGACAGATCGACGCTGCCATGCTGATTAATGACGCTCC 72
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagacacagcgtacgt 120
Db 71 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACTTACACAAACA 12
QY 121 t 121
Db 11 T 11
```

```
RESULT 36
US-09-865-419A-34794/C
Sequence 34794, Application US/09865419A
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(51935)B
CURRENT APPLICATION NUMBER: US/09/865,419A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/208,063
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 54020
SEQ ID NO 34794
LENGTH: 607
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3600-034-Q6-N6-F9
US-09-865-419A-34794
```

```
Query Match
Best Local Similarity 47.7%; Score 112; DB 33; Length 607;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgccatgctgtataatgagcgctcc 60
Db 112 GTTTCCGCTAGCCCTCGGTGGACAGATCGACGCTGCCATGCTGATTAATGACGCTCC 53
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagacacac 112
Db 52 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACACAC 1
```

```
RESULT 37
US-60-208-063-17853/C
Sequence 17853, Application US/60208063
GENERAL INFORMATION:
APPLICANT: Andersen, Scott E.
APPLICANT: Conner, Timothy W.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Lajudi, Raghunath V.
```

```
APPLICANT: Ruff, Thomas G.
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Wu, Kunsheng
APPLICANT: Xu, Nanfei
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
FILE REFERENCE: 38-21(51935)A
CURRENT APPLICATION NUMBER: US/60/208,063
CURRENT FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 25021
SEQ ID NO 17853
LENGTH: 607
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: LIB3600-034-Q6-N6-F9
US-60-208-063-17853
```

```
Query Match
Best Local Similarity 47.7%; Score 112; DB 59; Length 607;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgccatgctgtataatgagcgctcc 60
Db 112 GTTTCCGCTAGCCCTCGGTGGACAGATCGACGCTGCCATGCTGATTAATGACGCTCC 53
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagacacac 112
Db 52 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACACAC 1
```

```
RESULT 38
US-09-865-439A-6402/C
Sequence 6402, Application US/09865439A
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(51936)B
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 6402
LENGTH: 375
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3205-076-P1-N1-F7
US-09-865-439A-6402
```

```
Query Match
Best Local Similarity 47.4%; Score 111.4; DB 33; Length 375;
Matches 115; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgccatgctgtataatgagcgctcc 60
Db 133 GTTTCCGCTAGCCCTCGGTGGACAGATCGACCTGCCATGCTGATTAATGAGCGCTCC 74
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagacacacgctacgt 120
Db 73 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACACACCGCTCCGT 14
QY 121 t 121
Db 13 T 13
```

```
RESULT 39
```

```
US-09-865-439A-105057/c
; Sequence 105057, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 105057
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3608-030-Q6-N6-F9
US-09-865-439A-105057
```

```
Query Match          47.4%; Score 111.4; DB 33; Length 494;
Best Local Similarity 95.0%; Pred. No. 1e-25;
Matches 115; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 1 gtttcgctagcctcggtggaagatcgacgctgcccatgctgataaattgagcgtcc 60
Db 121 GTTTCCGCTCTAGCCCGCGGTCCAGATCGACGCTGCCCATGTTGATTAATGACGGTCC 62
OY 61 tgatccattgtcgtgtgtatataatgctgtataattgagcagacaacacagctacgt 120
Db 61 TGATCCATTGTCGTTGTTGTTATTAATGTTGTTAATTGACGACGACCAACACGTCGCT 2
OY 121 t 121
Db 1 T 1
```

```
RESULT 40
US-60-207-458-148977/c
; Sequence 148977, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 148977
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3608-030-Q6-N6-F9
US-60-207-458-148977
```

```
Query Match          47.4%; Score 111.4; DB 59; Length 494;
Best Local Similarity 95.0%; Pred. No. 1e-25;
Matches 115; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 1 gtttcgctagcctcggtggaagatcgacgctgcccatgctgataaattgagcgtcc 60
Db 121 GTTTCCGCTCTAGCCCGCGGTCCAGATCGACGCTGCCCATGTTGATTAATGACGGTCC 62
OY 61 tgatccattgtcgtgtgtatataatgctgtataattgagcagacaacacagctacgt 120
Db 61 TGATCCATTGTCGTTGTTGTTATTAATGTTGTTAATTGACGACGACCAACACGTCGCT 2
OY 121 t 121
Db 1 T 1
```

```
RESULT 41
US-60-207-458-50308/c
; Sequence 50308, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 50308
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb73301907a1
US-60-207-458-50308
```

```
Query Match          47.0%; Score 110.4; DB 59; Length 459;
Best Local Similarity 99.1%; Pred. No. 2.2e-25;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 gtttcgctagcctcggtggaagatcgacgctgcccatgctgataaattgagcgtcc 60
Db 112 GTTTCCGCTCTAGCCCGCGGTCCAGATCGACGCTGCCCATGTTGATTAATGACGGTCC 53
OY 61 tgatccattgtcgtgtgtatataatgctgtataattgagcagacaacacac 112
Db 52 TGATCCATTGTCGTTGTTGTTATTAATGTTGTTAATTGACGACGACCAAC 1
```

```
RESULT 42
US-09-865-439A-4731/c
; Sequence 4731, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 4731
```

```

; LENGTH: 257
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3205-056-P1-N1-B5
US-09-865-439A-4731

```

```

Query Match          46.5%; Score 109.2; DB 33; Length 257;
Best Local Similarity 71.7%; Pred. No. 4.5e-25;
Matches 114; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```

```

OY 1 gtttcgctagcctcggctggacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 199 GTTTCCGCTAGCGCTCGTGGGCAATTAACCGCTGCCATGCTAATAATGACGCTCC 140
    |||||||

OY 61 tgatccatgttcgctgtgttatttaattgataatgagcagacacacgctagct 120
    |||||||
DB 139 TGACCATGTTCGCTGTGTATTATGTAATGATGAGCAGACACACGCTAGCGT 80
    |||||||

OY 121 tnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 159
    |
DB 79 TACCCCTGTCTGTGTGTGTGTTGCATGCGCATGTCTC 41
    |

```

```

RESULT 43
US-09-865-439A-6464/c
; Sequence 6464, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 6464
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3205-078-P1-N1-D11
US-09-865-439A-6464

```

```

Query Match          43.3%; Score 101.8; DB 33; Length 391;
Best Local Similarity 90.1%; Pred. No. 1.4e-22;
Matches 109; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

OY 1 gtttcgctagcctcggctggacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 138 GTTTCCGCTAGCGCTCGTGGGCAATTAACCGCTGCCATGCTAATAATGACGCTCC 79
    |||||||

OY 61 tgatccatgttcgctgtgttatttaattgataatgagcagacacacgctagct 120
    |||||||
DB 78 TGATCCATGTTCGCTGTGTATTATGTAATGATGAGCAGACACGCTAGCTAGT 19
    |||||||

OY 121 t 121
    |
DB 18 T 18
    |

```

```

RESULT 44
US-60-207-458-42142/c
; Sequence 42142, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Delkman, Jill

```

```

; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lajudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 42142
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb73065g11a1
US-60-207-458-42142

```

```

Query Match          40.8%; Score 95.8; DB 59; Length 446;
Best Local Similarity 93.5%; Pred. No. 1.4e-20;
Matches 100; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

OY 1 gtttcgctagcctcggctggacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 107 GTTTCCGCTAGCGCTCGTGGGCAATTAACCGCTGCCATGCTAATAATGACGCTCC 48
    |||||||

OY 61 tgatccatgttcgctgtgttatttaattgataatgagcagac 107
    |||||||
DB 47 TGACCATGTTCGCTGTGTATTATGTAATGATGAGCAGGCC 1
    |

```

```

RESULT 45
US-09-692-257A-2923
; Sequence 2923, Application US/09692257A
; GENERAL INFORMATION:
; APPLICANT: Miller, Phillip W.
; APPLICANT: Peng, Ming
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15771)B
; CURRENT APPLICATION NUMBER: US/09/692,257A
; CURRENT FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/162,747
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 14882
; SEQ ID NO 2923
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-015-Q1-K1-C12
US-09-692-257A-2923

```

```

Query Match          34.8%; Score 81.8; DB 27; Length 382;
Best Local Similarity 92.5%; Pred. No. 5.2e-16;
Matches 86; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

OY 1 gtttcgctagcctcggctggacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 271 gtttcgctagcctcggctggacagatcgacgctgccatgctgataatgagcgctcc 330
    |||||||

OY 61 tgatccatgttcgctgtgttatttaattgataatgagcgta 93
    |||||||
DB 331 tgatccatgttcgctgtgttatttaattgataatgagcgta 363
    |||||||

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Tue Aug 20 07:55:45 2002

us-09-198-779b-1.rmpm

Page 15

Search completed: August 20, 2002, 02:32:18  
Job time: 7567 sec

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QY 221 aggtgtgtaagccccc 235  
|||||  
Db 1938 aggtgtgtaagccccc 1952

RESULT 10  
US-09-975-254-28588  
; Sequence 28588, Application US/09975254  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(15309)B  
; CURRENT APPLICATION NUMBER: US/09/975,254  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US/09/263,191  
; NUMBER OF SEQ ID NOS: 31255  
; SEQ ID NO 28588  
; LENGTH: 246  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700898670H1  
US-09-975-254-28588

Query Match 20.8%; Score 48.8; DB 5; Length 246;  
Best Local Similarity 77.6%; Pred. No. 5, 6e-07;  
Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 160 aggttcatcaagccgcgcatacgccacttggccggtgaagcgcgcacttcaactgc 219  
|||||  
Db 9 aggttcttcaagcagcgtcttatgacacttggaaaggtacacttcaactcctgc 68  
QY 220 gaggtgtcaagccccc 235  
|||||  
Db 69 gaggtgtgaagccac 84

RESULT 11  
US-09-975-254-31242  
; Sequence 31242, Application US/09975254  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(15309)B  
; CURRENT APPLICATION NUMBER: US/09/975,254  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US/09/263,191  
; NUMBER OF SEQ ID NOS: 31255  
; SEQ ID NO 31242  
; LENGTH: 259  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700902482H1  
US-09-975-254-31242

Query Match 20.8%; Score 48.8; DB 5; Length 259;  
Best Local Similarity 75.7%; Pred. No. 5, 7e-07;  
Matches 56; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 159 caggttcatcaagccgcgcatacgccacttggccggtgaagcgcgcacttcaactgc 218  
|||||  
Db 142 caggttcttcaagcagcgtcttatgacacttggaaaggtacacttcaactcctgc 201

QY 219 cgaggtgtgtcaagc 232  
|||||  
Db 202 ggaantgttgaagc 215

RESULT 12  
US-09-424-978B-40  
; Sequence 40, Application US/09424978B  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafalski, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424,978B  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/048,771  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 1479  
; TYPE: DNA  
; ORGANISM: Lycopersicon esculentum  
US-09-424-978B-40

Query Match 20.8%; Score 48.8; DB 5; Length 1479;  
Best Local Similarity 77.6%; Pred. No. 9, 9e-07;  
Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 160 aggttcatcaagccgcgcatacgccacttggccggtgaagcgcgcacttcaactgc 219  
|||||  
Db 1200 aggttcttgaagcagcgtcttatgacacttggaaaggtacacttcaactcctgc 1259  
QY 220 gaggtgtcaagccccc 235  
|||||  
Db 1260 gaggtgtgaagccccc 1275

RESULT 13  
US-10-155-881-37534  
; Sequence 37534, Application US/10155881  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(13500)J  
; CURRENT APPLICATION NUMBER: US/10/155,881  
; PRIOR FILING DATE: 2002-05-22  
; NUMBER OF SEQ ID NOS: 37534  
; SEQ ID NO 37534  
; LENGTH: 1940  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-155-881-37534

Query Match 20.8%; Score 48.8; DB 7; Length 1940;  
Best Local Similarity 77.6%; Pred. No. 1, 1e-06;  
Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 160 aggttcatcaagccgcgcatacgccacttggccggtgaagcgcgcacttcaactgc 219  
|||||  
Db 1614 aggttcttcaagcagcgtcttatgacacttggaaaggtacacttcaactcctgc 1673

QY	220	gaagtgtg	caagcccc	235
Db	1674	gaagttgt	gaagccac	1689

```

RESULT 14
US-09-975-254-980
; Sequence 980, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 980
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700732290H1
US-09-975-254-980

```

Query Match	20.5%	Score 48.2	DB 5	Length 246
Best Local Similarity	76.6%	Pred. No. 9.1e-07		
Matches	59	Conservative	0	Mismatches 18
				Indels 0
				Gaps 0
QY 159	caggtctatcaagaccgcgcataagccattgcccgttaacagacgcgaattactctg	218		
Db 87	caggttttggaactcgtgcctatcagcactttggaagagaagaccctgattccatctg	146		
QY 219	cgaggtggtcaagcccc	235		
Db 147	ggaagtgtgtcaaacccc	163		

```

RESULT 15
US-09-975-254-956
: Sequence 956, Application US/09/975254
: GENERAL INFORMATION:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: Heck, Gregory R.
: APPLICANT: La Rosa, Thomas J.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(15309)P
: CURRENT APPLICATION NUMBER: US/09/975,254
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US/09/263,191
: PRIOR FILING DATE: 1999-03-05
: NUMBER OF SEQ ID NOS: 31255
: SEQ ID NO 956
: LENGTH: 251
: TYPE: DNA
: ORGANISM: Glycine max
: OTHER INFORMATION: Clone ID: 700732265H1
US-09-975-254-956

```

Query Match	20.5%	Score 48.2	DB 5	Length 251
Best Local Similarity	76.6%	Pred. No. 9.1e-07		
Matches 59	Conservative 0	Mismatches 18	Indels 0	Gaps 0
0y	159	caggttcaacagaccgcgcataagcgcacttggccctgagcagccgcgaattcactg	218	
db	87	caggttttgaagactgtcctctcagcagcactttggaagaaagacccttcactacatg	146	

QY	219	cgaggtggtcaagccc	235
Db	147	ggaagtgtcaaacccc	163

```

RESULT 16
US-09-975-254-26838
; Sequence 26838, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 26838
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700896326H1
US-09-975-254-26838

```

	Query Match	Similarity	Score	DB	Length
Best Local	59	76.6%	20.5%	5	258
Matches	59	Conservative	0	Mismatches	18
				Indels	0
				Gaps	0
QY	159	caggtcaacgaacgcgcgcataagccactttgcgctgacgagccgacttaccctg	218		
Db	152	caggttttgaagactgcctgactatgacacttggaaagagaagaccctgacttcatg	211		
QY	219	cgaggtggtcaaacgcc	235		
Db	212	ggaagtgtgccaacccc	228		

```

RESULT 17
US-09-975-254-14222
; Sequence 14222, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 14222
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700908822H1
US-09-975-254-14222

```

Query Match	Similarity	Score	DB	Length
Best Local	Similarity 76.0%	Pred No. 4.6e-06		
Matches	57; Conservative	0; Mismatches	18; Indels	0; Gaps
QY	161 ggttcatacaagacgcgcgatacggcaccattggccgtgaagacgcgcgaattaccctgcg		220	
Db	1 ggttttttgaagactcgtcgtctatgaacacttttgaagaagaacccctgattccatcattgg		60	
QY	221 aggtgtgtcaagcccc		235	









```

; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 44755
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: SYNECHOCOCCUS SP. WH 8102
US-60-360-039-44755

Query Match               13.0%; Score 30.6; DB 8; Length 1158;
Best Local Similarity    73.6%; Pred. No. 2;
Matches   39; Conservative     0; Mismatches   14; Indels     0; Gaps     0;

QY      170 agaccgcgcatagcgaacttggccgttagacagcgcaacttcacctgcgag 222
          ||| |||| | |||| |||| || ||| |||| | | | ||| |||
Db       1106 acacagcgcttaaggcacttgctgcgtatagaacattaacgcccttgtgag 1158

RESULT 33
US-60-360-039-43390
; Sequence 43390, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 43390
LENGTH: 1161
TYPE: DNA
ORGANISM: Nitrosomonas europaea
US-60-360-039-43390

Query Match              13.0%; Score 30.6; DB 8; Length 1161;
Best Local Similarity    42.5%; Pred. No. 2;
Matches   45; Conservative     0; Mismatches   61; Indels     0; Gaps     0;

QY      116 taagtlnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncagttcataagacg 175
           |||| 
Db       1013 taagcctcgggccatcacgaactgatctgctgcatttatgcaaaacg 1072

QY      176 ccgatacggcaacttggccgttagacagcgcaacttcacctgcga 221
           | ||| | | | | | | | | | | | | | | | | | | | | |
Db       1073 ctgctatgcatlcttggccgggaagaaccagcatttaccytgga 1118

RESULT 34
US-60-360-039-33893
; Sequence 33893, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 33893
LENGTH: 3540
TYPE: DNA
ORGANISM: Cytophaga hutchinsonii
US-60-360-039-33893
```

; ORGANISM: magnetite-containing magnetic coccus

Matches 52; Con

Matches	52;	Conservative	0;	Mismatches	19;	Indels	1;	Gaps	1;
---------	-----	--------------	----	------------	-----	--------	----	------	----

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    QY      58 tccgatcattgttcgltgtaataatgttataattgcagacgaacaacgta 117
              ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db         114 TCCCAAAAGGTGTTGGTATGATTATTAATTTTCCTFAAAGAGAAGTCACAAAGTTTA 55
QY      118 cgtctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnca 160
              | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db         54 TGATTAATATATTNTAATGATCATCACTTAACCTTGAGATTGACAGGA 12

RESULT 41
US-10-027-632-215532
; Sequence 215532, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10-/027, 632
; PRIORITY FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215532
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215532

Query Match          12.4%: Score 29.2; DB 7; Length 548;
Best Local Similarity 42.7%; Pred. No. 4.9;
Matches 44; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY      58 tccgatcattgttcgltgtaataatgttataattgcagacgaacaacgta 117
              ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db         114 TCCCAAAAGGTGTTGGTATGATTATTAATTTTCCTFAAAGAGAAGTCACAAAGTTTA 55
QY      118 cgtctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnca 160
              | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db         54 TGATTAATATATTNTAATGATCATCACTTAACCTTGAGATTGACAGGA 12

US-10-027-632-215532
; Sequence 215532, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10-/027, 632
; PRIORITY FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215532
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215532

Query Match          12.4%: Score 29.2; DB 7; Length 650;
Best Local Similarity 41.4%; Pred. No. 5.2;
Matches 46; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY      58 tccgatcattgttcgltgtaataatgttataattgcagacgaacaacgta 117
              ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db         373 tccgatcattgcagtgcctctccatattgtttaattgtaaaagaacacttt 432

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Date: Aug 20, 2002 2:58 AM  
About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
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-Q/cgn2\_1/USPTO.spool/US09198779/runat.19082002.140912.2510/app-query.fasta.1.296  
-DB=PIR\_71 -OFMT=fastan -SUFFIX=pr -GAPO=12.000 -GAPEXT=4.500  
-MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000 -OGAPO=4.500  
-OGAPEXT=0.050 -XGAPO=10.000 -XGAPEXT=0.500 -FGAPO=6.000  
-FGAPEXT=7.000 -YGAPO=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blissum62 -TRANS=human4.0.cdi  
-ALIGN=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
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-NO\_XLPXY -WAIT -THREADS=1

Search information block:  
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Query Length: 235  
Database: PIR\_71.\*  
Database sequences: 283138  
Database length: 96089334  
Search time (sec): 33.210000

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Sequence Strd Orig ZScore EScore Len Documentation  
PIR2:T06180 + 127.00 320.35 2.4e-10 394 methionine adenosyltransferase  
PIR2:P00817 + 120.00 315.63 2.5e-09 68 methionine adenosyltransferase  
PIR2:J00131 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase  
PIR2:S38875 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase  
PIR2:S46538 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase  
PIR2:C66155 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase  
PIR2:T06592 + 116.00 291.14 1.1e-08 360 methionine adenosyltransferase  
PIR2:S66351 + 116.00 291.01 1.1e-08 360 methionine adenosyltransferase  
PIR2:G64785 + 113.00 287.77 1.6e-08 390 probable s-adenosylmethionine s  
PIR2:J00410 + 115.00 287.70 1.6e-08 393 methionine adenosyltransferase  
PIR2:S66352 + 108.50 269.93 1.5e-07 397 methionine adenosyltransferase  
PIR2:T07899 + 101.00 256.02 2.0e-06 179 methionine adenosyltransferase  
PIR2:S49431 + 101.00 249.66 2.1e-06 390 methionine adenosyltransferase  
PIR2:S46540 + 101.00 249.66 2.1e-06 390 methionine adenosyltransferase  
PIR2:T10710 + 98.00 241.37 6.0e-06 396 methionine adenosyltransferase  
PIR2:G72228 + 74.00 176.07 0.0260 389 s-adenosylmethionine synthetase  
PIR2:EB1986 + 72.00 170.75 0.0522 389 probable methionine adenosyltr  
PIR2:DB1042 + 72.00 170.75 0.0522 389 s-adenosylmethionine synthetase  
PIR2:SS1671 + 68.00 159.88 0.2107 388 methionine adenosyltransferase  
PIR2:DB9657 + 65.00 151.47 0.6014 400 methionine adenosyltransferase  
PIR2:BB7255 + 64.50 149.96 0.7166 407 s-adenosylmethionine synthetase  
PIR2:AB2895 + 64.00 149.25 0.8501 376 s-adenosylmethionine synthetase  
PIR2:J00059 + 63.50 134.33 1.09 1979 metpd protein - mouse  
PIR1:S72257 + 63.00 146.13 1.21 395 methionine adenosyltransferase  
PIR2:A27118 + 63.00 145.96 1.21 395 methionine adenosyltransferase  
PIR2:HB6976 + 63.00 145.96 1.21 403 probable s-adenosylmethionine s  
PIR2:G87485 + 63.00 142.88 1.23 589 hypothetical protein CC1908 [lm  
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PIR2:BE4544 + 61.00 140.89 2.43 385 methionine adenosyltransferase  
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PIR2:AH1282 + 61.00 140.52 2.43 399 probable metk protein - Mycobac  
PIR2:FT0899 + 61.00 140.48 2.44 403 methionine adenosyltransferase  
PIR2:BB7403 + 61.00 140.18 2.44 420 s-adenosylmethionine synthetase  
PIR2:AB2621 + 61.00 134.17 2.52 877 heme transport protein alr3242  
PIR2:AC2211 + 60.50 139.04 2.90 409 methionine adenosyltransferase

PIR2:EB2319 + 60.00 138.17 3.44 385 s-adenosylmethionine syntha  
PIR2:BB4381 - 60.00 133.60 3.53 674 acylaminoacyl-peptidase [lm  
PIR2:A71281 + 59.00 135.22 4.88 396 probable s-adenosylmethionit  
PIR2:A47151 + 59.00 135.22 4.88 396 methionine adenosyltransfer  
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seq\_documentation\_block:  
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N:Alternate names: S-adenosylmethionine synthetase  
C:Species: Hordeum vulgare (barley)  
C>Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 20-Jun-2000  
C:Accession: T06180  
R:Morris S  
submitted to the EMBL Data Library, August 1995  
A:Reference number: Z15512  
A:Accession: T06180  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-394 <MOR>  
A:Cross-references: EMBL:D63835; PIDN:BA09895.1  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase  
alignment\_scores:  
Quality: 127.00 Length: 25  
Ratio: 5.292 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 96.000  
alignment\_block:  
US-09-198-779b-1 x T06180 ..  
Align seg 1/1 to: T06180 from: 1 to: 394  
160 AGGTTTCATCAAGACCGCGCATACGCGCACTTGCGCGTGACGACCGCA 209  
|||||  
362 ATGPhetIleIyStHrAlAlAtyTcGlyHnPhetGlyATGAspAspAlaAs 378  
210 CTTGACCTGCGAGGTGCTCAAGCC 234  
|||||  
378 PPhetHrTgPgluValValysPro 386  
seq\_name: PIR2:P00817  
seq\_documentation\_block:  
M:Alternate names: adenosyltransferase (EC 2.5.1.6) - rape (fragment)  
C:Species: Brassica napus (rape)  
C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 05-May-2000  
C:Accession: P00817  
R:Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam  
Plant Physiol. 103, 359-370, 1993  
A:Title: Generation of expressed sequence tags of random root cDNA clones of Brassica  
A:Reference number: P00816; MUID:94302145  
A:Accession: P00817  
A:Molecule type: mRNA  
A:Residues: 1-68 <PAR>  
A:Experimental source: root, cv. Naeahan  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase  
alignment\_scores:  
Quality: 120.00 Length: 25  
Ratio: 5.217 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 88.000  
alignment\_block:  
US-09-198-779b-1 x P00817 ..  
Align seg 1/1 to: P00817 from: 1 to: 68

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209  
 |||||||:||||||||||||||||||||||||||||||||||||| 11  
 36 ArgpHeuLeuYstHrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 52  
 210 CTTACACCTGCGAGGTGTCAAGCCC 234  
 ||||||| |||||||  
 52 pPheHrTrpGluValValLysPro 60

seq\_name: p1r2:JN0131

seq\_documentation\_block:

methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana  
 N:Alternate names: S-adenosyl-L-methionine synthetase  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 05-May-2000  
 C:Accession: JN0131  
 R:Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Botterman, J.; Alliotte, T.; Van M  
 Plant Cell 1, 81-93, 1989  
 A:Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop  
 A:Reference number: JN0131; MUID:92386056  
 A:Accession: JN0131  
 A:Molecule type: DNA  
 A:Residues: 1-393 <PEL>  
 A:Cross-references: GB:M55077; NID:g166871; PIDN:AAA32868.1; PID:g166872  
 A:Experimental source: var. K85  
 A:Note: the sequence derived from var. Columbia differs from that shown in having 117-Gl  
 C:Comment: S-adenosylmethionine synthetase catalyzes the biosynthesis of adenosylmethio  
 C:Genetics:  
 A:Gene: sam-1  
 C:Superfamily: methionine adenosyltransferase  
 C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
 Quality: 120.00 Length: 25  
 Ratio: 5.217 Gaps: 0  
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:  
 US-09-198-779B-1 x JN0131 ..

Align seg 1/1 to: JN0131 from: 1 to: 393

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209  
 |||||||:||||||||||||||||||||||||||||||||||||| 11  
 361 ArgpHeuLeuYstHrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377  
 210 CTTACACCTGCGAGGTGTCAAGCCC 234  
 ||||||| |||||||  
 377 pPheHrTrpGluValValLysPro 385

seq\_name: p1r2:S38875

seq\_documentation\_block:

methionine adenosyltransferase (EC 2.5.1.6) - tomato  
 N:Alternate names: S-adenosyl-L-methionine synthetase  
 C:Species: Lycopersicon esculentum (tomato)  
 C>Date: 22-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-May-2000  
 C:Accession: S46539; S38875  
 R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.  
 Plant Mol. Biol. 25, 217-227, 1994  
 A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res  
 A:Reference number: S46539; MUID:94289646  
 A:Accession: S46539  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <ES2>  
 A:Cross-references: EMBL:Z24742; NID:g429105; PIDN:CAA80866.1; PID:g429106  
 C:Superfamily: methionine adenosyltransferase  
 C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
 Quality: 120.00 Length: 25  
 Ratio: 5.217 Gaps: 0  
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:  
 US-09-198-779B-1 x S38875 ..

Align seg 1/1 to: S38875 from: 1 to: 393

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209  
 |||||||:||||||||||||||||||||||||||||||||||||| 11  
 361 ArgpHeuLeuYstHrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377  
 210 CTTACACCTGCGAGGTGTCAAGCCC 234  
 ||||||| |||||||  
 377 pPheHrTrpGluValValLysPro 385

seq\_name: p1r2:S46538

seq\_documentation\_block:

methionine adenosyltransferase (EC 2.5.1.6) - tomato  
 N:Alternate names: S-adenosyl-L-methionine synthetase  
 C:Species: Lycopersicon esculentum (tomato)  
 C>Date: 26-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-May-2000  
 C:Accession: S46538; S38874  
 R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.  
 Plant Mol. Biol. 25, 217-227, 1994  
 A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in  
 A:Reference number: S46538; MUID:94289646  
 A:Accession: S46538  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <ESP>  
 A:Cross-references: EMBL:Z24741; NID:g429103; PIDN:CAA80865.1; PID:g429104  
 C:Superfamily: methionine adenosyltransferase  
 C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
 Quality: 120.00 Length: 25  
 Ratio: 5.217 Gaps: 0  
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:  
 US-09-198-779B-1 x S46538 ..

Align seg 1/1 to: S46538 from: 1 to: 393

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209  
 |||||||:||||||||||||||||||||||||||||||||||||| 11  
 361 ArgpHeuLeuYstHrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377  
 210 CTTACACCTGCGAGGTGTCAAGCCC 234  
 ||||||| |||||||  
 377 pPheHrTrpGluValValLysPro 385

seq\_name: p1r2:C86155

seq\_documentation\_block:

S-adenosylmethionine synthetase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: C86155  
 R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
 ansen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallo  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.





```

|||||  |||||||
377 pPheHrTrpGluValValysPro 385
seq_name: p1r2:J00410

```

```

seq_documentation_block:
  methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-May-2000
C:Accession: J00410
R:Peteman, J.; Salto, K.; Collyn, B.; Engler, G.; Seurinck, J.; Van Montagu, M.; Inze, D
Gene 84, 359-369, 1989
A:Title: Structure and expression analyses of the S-adenosylmethionine synthetase gene
A:Reference number: J00410; MUID:90128280
A:Accession: J00410
A:Molecule type: DNA
A:Residues: 1-393 <PEL>
A:Cross-references: GB:M33217; NID:g166873; PIDN:AAA32869.1; PID:g166874
C:Genetics:
A:Gene: sam-2
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

```

```

alignment_scores:
  Quality: 115.00      Length: 25
  Ratio: 5.227        Gaps:
  Percent Similarity: 88.000      Percent Identity: 88.000

```

```

alignment_block:
US-09-198-779B-1 x J00410 ..

```

```

Align seg 1/1 to: J00410 from: 1 to: 393

```

```

160 AGGTCATCAAGACCGCCGATACGGCCACTTGGCCGTGACGACGCCGA 209
|||||  |||||||
361 ArgPheGluLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACTGCGAGGTGTCAGGCC 234
|||||  |||||||
377 pPheHrTrpGluValValysPro 385

```

```

seq_name: p1r2:S66352

```

```

seq_documentation_block:
  methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C:Accession: S66352; S52218
R:Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A:Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries
A:Reference number: S66351; MUID:96194463
A:Accession: S66352
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-397 <GOM>
A:Cross-references: EMBL:X82077
R:Gomez, L.; Carrasco, P.
Submitted to the EMBL Data Library, October 1994
A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries.
A:Reference number: S52218
A:Accession: S52218
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364, 'FEDSCITWF' <GOM>
A:Cross-references: EMBL:X82077; NID:g609224; PIDN:CAA57581.1; PID:g609225
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

```

```

alignment_scores:

```

```

Quality: 108.50      Length: 26
Ratio: 4.717        Gaps: 1
Percent Similarity: 88.462      Percent Identity: 84.615

```

```

alignment_block:
US-09-198-779B-1 x S66352 ..

```

```

Align seg 1/1 to: S66352 from: 1 to: 397

```

```

160 AGGTC...ATCAAGACCGCCGATACGGCCACTTGGCCGTGACGACGC 206
|||||  |||||||
363 ArgPheGluLeuLysThrAlaAlaTyrGlyHisPheGlySerAspAspAl 379
207 CGACTTCACCTCGCAGGTGTCAGGCC 234
|||||  |||||||
379 aAspPheHrTrpGluValValysPro 388

```

```

seq_name: p1r2:T07899

```

```

seq_documentation_block:
  methionine adenosyltransferase (EC 2.5.1.6) - Chlamydomonas reinhardtii (fragment)
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Chlamydomonas reinhardtii
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-May-2000
C:Accession: T07899
R:Kim, J.Y.; Lee, K.O.; Lee, S.H.
Submitted to the EMBL Data Library, June 1997
A:Description: Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase.
A:Reference number: Z16198
A:Accession: T07899
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-179 <KIM>
A:Cross-references: EMBL:AF008568; NID:g2454483; PIDN:AAB71833.1; PID:g2454484
A:Experimental source: strain 137C
C:Genetics:
A:Gene: SAMS
C:Function:
A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and py
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

```

```

alignment_scores:
  Quality: 101.00      Length: 24
  Ratio: 4.810        Gaps: 0
  Percent Similarity: 87.500      Percent Identity: 79.167

```

```

alignment_block:
US-09-198-779B-1 x T07899 ..

```

```

Align seg 1/1 to: T07899 from: 1 to: 179

```

```

160 AGGTCATCAAGACCGCCGATACGGCCACTTGGCCGTGACGACGCCGA 209
|||||  |||||||
153 ArgTyrGluLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 169
210 CTTCACTGCGAGGTGTCAG 231
|||||  |||:|||||
169 pPheHrTrpGluThrValys 176

```

```

seq_name: p1r2:S49491

```

```

seq_documentation_block:
  methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C>Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C:Accession: S49491
R:Iznaki, A.; Shoseyov, O.; Weiss, D.
Submitted to the EMBL Data Library, October 1994
A:Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
A:Reference number: S49491
A:Accession: S49491

```

A:Molecule type: mRNA  
A:Residues: 1-390 <I2H>  
A:Cross-references: EMBL:X82214; NID:g5559505; PIDN:CAA57696.1; PID:g5559506  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
Quality: 101.00 Length: 24  
Ratio: 4.810 Gaps: 0  
Percent Similarity: 87.500 Percent Identity: 79.167

alignment\_block:  
US-09-198-779B-1 x S49491 ..

Align seg 1/1 to: S49491 from: 1 to: 390

```
160 AGTTTCATCAAGACCGCGCATACGGCCATTGGCCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCAG 231
||||| ||||||| ||||||| ||||||| ||
377 pPheThrTrpGlnThrValLys 384
```

seq\_name: p1r2:S46540

seq\_documentation\_block:  
methionine adenosyltransferase (EC 2.5.1.6) - tomato  
N:Alternate names: S-adenosyl-L-methionine synthetase  
C:Species: Lycopersicon esculentum (tomato)  
C>Date: 26-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-May-2000  
R:Accession: S46540; S38876  
R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.  
Plant Mol. Biol. 25, 217-227, 1994  
A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res  
A:Reference number: S46538; MUID:94289646  
A:Accession: S46540  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-390 <ESP>  
A:Cross-references: EMBL:Z24743; NID:g429107; PIDN:CAA80867.1; PID:g429108  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
Quality: 101.00 Length: 24  
Ratio: 4.810 Gaps: 0  
Percent Similarity: 87.500 Percent Identity: 79.167

alignment\_block:  
US-09-198-779B-1 x S46540 ..

Align seg 1/1 to: S46540 from: 1 to: 390

```
160 AGTTTCATCAAGACCGCGCATACGGCCATTGGCCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCAG 231
||||| ||||||| ||||||| ||||||| ||
377 pPheThrTrpGlnThrValLys 384
```

seq\_name: p1r2:T10710

seq\_documentation\_block:  
methionine adenosyltransferase (EC 2.5.1.6) - clove pink  
N:Alternate names: S-adenosylmethionine synthetase  
C:Species: Dianthus caryophyllus (clove pink)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 05-May-2000  
C:Accession: T10710  
R:Larsen, P.B.; Woodson, W.R.

submitted to the EMBL Data Library, April 1991  
A:Description: Cloning and nucleotide sequence of a S-adenosylmethionine synthetase  
A:Reference number: Z17091  
A:Accession: T10710  
A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-396 <LAR>  
A:Cross-references: EMBL:M61882; NID:g167961; PID:g304637  
C:Genetics:  
A:Gene: SAM2  
C:Function:  
A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and p  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
Quality: 98.00 Length: 24  
Ratio: 4.455 Gaps: 0  
Percent Similarity: 91.667 Percent Identity: 70.833

alignment\_block:  
US-09-198-779B-1 x T10710 ..

Align seg 1/1 to: T10710 from: 1 to: 396

```
160 AGTTTCATCAAGACCGCGCATACGGCCATTGGCCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
364 ArgTyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAs 380
210 CTTACCTGCGAGGTGTCAG 231
||||| ||||||| ||||||| ||||||| ||
380 pPheThrTrpGlnThrAlaLys 387
```

seq\_name: p1r2:G72228

seq\_documentation\_block:  
S-adenosylmethionine synthetase - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: G72228  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.V.; Haft, D.H.; Hix  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,  
C.M.

Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A:Reference number: A72200; MUID:99287316

A:Accession: G72228  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <ARN>  
A:Cross-references: GB:AE001807; GB:AE000512; NID:g4982216; PIDN:ABD36725.1; PID:g49.  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TMI658  
C:Superfamily: methionine adenosyltransferase

alignment\_scores:  
Quality: 74.00 Length: 18  
Ratio: 4.625 Gaps: 0  
Percent Similarity: 88.889 Percent Identity: 72.222

alignment\_block:  
US-09-198-779B-1 x G72228 ..

Align seg 1/1 to: G72228 from: 1 to: 395

```
169 AAGACCGCGCATACGGCCATTGGCCGTGACGACGCCGACTACCTG 218
||||| ||||||| ||||||| ||||||| ||||||| ||
364 LysThrAlaAlaTyrGlyHisPheGlyArgAsnGluGlnThrThr 380
219 CGAG 222
```

111  
380 pglu 381  
seq\_name: p1r2:E81986

seq\_documentation\_block:

probable methionine adenosyltransferase (EC 2.5.1.6) NMA0663 [Imported] - Neisseria men  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: E81986  
R:Parhill, J.; Achman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z2491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: E81986  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-389 <PAR>  
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83950.1; PID:g737939  
A:Experimental source: serogroup A, strain z2491  
C:Genetics:  
A:Gene: metK: NMA0663  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:

Quality:	72.00	Length:	20
Ratio:	4.235	Gaps:	0
Percent Similarity:	85.000	Percent Identity:	60.000

alignment\_block:

US-09-198-779b-1 x E81986 ..

Align seg 1/1 to: E81986 from: 1 to: 389

```

163 TTTCATCAAGACCGCCGATACGCGCATTTGGCCGTGACGACGCGGACTT 212
    ::::::::::::::::::::::::::::::::::::::::::::
356 TysSerLysSerAlaAlaTyrGlyHisPheGlyArgGluInuProGluPh 372
213 CACCTGCGAG 222
    |||||
372 ethrTpglu 375

```

seq\_name: p1r2:D81042

seq\_documentation\_block:

S:adenosylmethionine synthetase NMB1799 [Imported] - Neisseria meningitidis (strain MC58  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: D81042  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.R.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
Li, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizze, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175735  
A:Accession: D81042  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-389 <RET>  
A:Cross-references: GB:AE002530; GB:AE002098; NID:g7227054; PIDN:AAF42136.1; PID:g722705  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1799  
C:Superfamily: methionine adenosyltransferase

alignment\_scores:

Quality:	72.00	Length:	20
Ratio:	4.235	Gaps:	0

Percent Similarity: 85.000 Percent Identity: 60.000

alignment\_block:

US-09-198-779b-1 x D81042 ..

Align seg 1/1 to: D81042 from: 1 to: 389

```

163 TTTCATCAAGACCGCCGATACGCGCATTTGGCCGTGACGACGCGGACTT 212
    ::::::::::::::::::::::::::::::::::::::::::::
356 TysSerLysSerAlaAlaTyrGlyHisPheGlyArgGluInuProGluPh 372
213 CACCTGCGAG 222
    |||||
372 ethrTpglu 375

```

seq\_name: p1r2:S51671

seq\_documentation\_block:

methionine adenosyltransferase (EC 2.5.1.6) - Acanthamoeba castellanii  
C:Species: Acanthamoeba castellanii  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-May-2000  
C:Accession: S51671  
R:Ahm, K.S.; Henney, H.  
submitted to the EMBL Data Library, May 1994  
A:Reference number: S51671  
A:Accession: S51671  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-388 <AHN>  
A:Cross-references: EMBL:X79205  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:

Quality:	68.00	Length:	21
Ratio:	4.250	Gaps:	0
Percent Similarity:	76.190	Percent Identity:	61.905

alignment\_block:

US-09-198-779b-1 x S51671 ..

Align seg 1/1 to: S51671 from: 1 to: 388

```

169 AAGACCGCCGATACGCGCATTTGGCCGTGACGACGCGGACTTACCTG 218
    |||||
364 LysThrAlaTyrHisGlyHisPheGlyArgGluInuProAspPheLeu 380
219 CGAGTGTGTGAC 231
    |||||
380 pgluAlaProLys 384

```

seq\_name: p1r2:D69657

seq\_documentation\_block:

methionine adenosyltransferase (EC 2.5.1.6) - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: D69657  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Calowell, B.; Capuano, V.; Carter, N.M.;  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma  
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scari  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstira, P.; Tsunomi, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipit, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.



## alignment\_scores:

Quality: 63.50 Length: 82  
 Ratio: 1.411 Gaps: 2  
 Percent Similarity: 54.878 Percent Identity: 24.390

## alignment\_block:

US-09-198-779B-1/rev x JW0059 ..

Align seg 1/1 to: JW0059 from: 1 to: 1979

```

228 GACCACCTCGAGTGAAGTCGCGCTGACGCGCAAGGCGCGTATG 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1382 AsphismetalaSerGluThrGlnIleLeuGlnAspThrIleuGlyValCy 1398
178 C.....:GGCGGTCTTCATGATAC 162
1398 sValAtgSerGlnGlySerAlaAlaAspAlaAspProAlaLeuSerGluP 1415
161 CTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAACGTACGTCG 112
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1415 roGluGlyAsnSerGluHisSerGlySerSerAspSer..... 1427
111 TTGTGCTCTGCTCAATTATACACATTAATACACACACATGATG 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1428 LeuTrpGlnAlaSerLeuGlnAsnValSerGlyThrThrAspAlaProAl 1444
61 AGACCGCTCATTTATTCAGCAGCGCGTCGATGTCACCGA 16
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1444 aaAlaProSerValAlaIleGlnValSerValSerMetValHisGln 1459
seq_name: pir1:S27257

```

## seq\_documentation\_block:

methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human  
 N:Alternate names: renal methionine adenosyltransferase (MAT); S-adenosylmethionine synt  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 11-Jun-1999  
 C:Accession: S27257  
 R:Horikawa, S.; Tsukada, K.  
 FEBS Lett. 312, 37-41, 1992  
 A:Title: Molecular cloning and developmental expression of a human kidney S-adenosylmeth  
 A:Reference number: S27257; MUID:93050159  
 A:Accession: S27257  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-395 <HOR>  
 A:Cross-references: EMBL:X68836; GB:S47859; NID:936326; PIDN:CAA48726.1; PID:936327  
 C:Genetics:  
 A:Gene: GDB:MAT2A; SAMS2; MAT2A  
 A:Cross-references: GDB:136213; OMIM:601468  
 A:Map position: 2p11.2-2p11.2  
 A:Introns: 15/2; 256/3  
 C:Complex: heterodimer of catalytic alpha and regulatory beta chains  
 C:Function:  
 A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyroP  
 A:Pathway: one-carbon metabolism  
 C:Superfamily: methionine adenosyltransferase  
 C:Keywords: ATP; heterodimer; kidney; magnesium; metalloprotein; one-carbon metabolism;  
 F:219-286/Region: nucleotide-binding motif A (P-loop) #status atypical  
 F:31/Binding site: magnesium 2 (Asp) #status predicted  
 F:285,289/Active site: Lys #status predicted  
 F:291/Binding site: magnesium 1 (Asp) #status predicted

## alignment\_scores:

Quality: 63.00 Length: 21  
 Ratio: 3.938 Gaps: 1  
 Percent Similarity: 76.190 Percent Identity: 66.667

## alignment\_block:

US-09-198-779B-1 x S27257 ..

Align seg 1/1 to: S27257 from: 1 to: 395

```

169 AAGACCGCGCATACGCGCATTTGGCCGTGACGACCGCGACTTCACCTG 218
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
373 ArgThrAlaAlaIleArgIleHisPheGlyArgAsp.....SerPheProTr 387
219 CGAGGTGTCACAG 231
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
387 pGluValProLys 391
seq_name: pir2:A37118

```

## seq\_documentation\_block:

methionine adenosyltransferase (EC 2.5.1.6) - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 15-Feb-1991 #sequence\_revision 15-Feb-1991 #text\_change 05-May-2000  
 C:Accession: A37118  
 R:Horikawa, S.; Sasuga, J.; Shimizu, K.; Ozasa, H.; Tsukada, K.  
 J. Biol. Chem. 265, 13683-13686, 1990  
 A:Title: Molecular cloning and nucleotide sequence of cDNA encoding the rat kidney S-  
 A:Reference number: A37118; MUID:90337979  
 A:Accession: A37118  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-395 <HOR>  
 A:Cross-references: GB:J05571; NID:9206845; PIDN:AAA42106.1; PID:9206846  
 C:Superfamily: methionine adenosyltransferase  
 C:Keywords: S-adenosylmethionine; transferase

## alignment\_scores:

Quality: 63.00 Length: 21  
 Ratio: 3.938 Gaps: 1  
 Percent Similarity: 76.190 Percent Identity: 66.667

## alignment\_block:

US-09-198-779B-1 x A37118 ..

Align seg 1/1 to: A37118 from: 1 to: 395

```

169 AAGACCGCGCATACGCGCATTTGGCCGTGACGACCGCGACTTCACCTG 218
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
373 ArgThrAlaAlaIleArgIleHisPheGlyArgAsp.....SerPheProTr 387
219 CGAGGTGTCACAG 231
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
387 pGluValProLys 391
seq_name: pir2:H86976

```

## seq\_documentation\_block:

probable S-adenosylmethionine synthase [imported] - Mycobacterium leprae  
 C:Species: Mycobacterium leprae  
 C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C:Accession: H86976  
 R:Cole, S.T.; Elgimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;  
 R.; Davies, R.M.; Devlin, K.; Dutboy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holto  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A:Authors: Rutherford, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;  
 A:Title: Massive gene decay in the leprosy bacillus.  
 A:Reference number: A86909; MUID:21128732; PMID:11234002  
 A:Accession: H86976  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-403 <STO>  
 A:Cross-references: GB:AL450380; NID:913092748; PIDN:CAC30052.1; GSPDB:GN00147  
 C:Genetics:  
 A:Gene: meck  
 C:Superfamily: methionine adenosyltransferase







C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
Quality: 61.00 Length: 18  
Ratio: 4.067 Gaps: 0  
Percent Similarity: 83.333 Percent Identity: 61.111

alignment\_block:  
US-09-198-779B-1 x F86862 ..

Align seg 1/1 to: F86862 from: 1 to: 399

```

169 AAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGACTTACCTG 218
      ::::::::::::::::::::::::::::::::::::
368 GlnThrAlaAlaPheGlyHisPheGlyArgThrAspValGluLeuProTr 384

219 CGAG 222
      |||
384 pGlu 385

```

seq\_name: p1r2:AD1654

seq\_documentation\_block:

S-methionine adenosyltransferase homolog metk [imported] - *Listeria innocua* (strain C11)  
C:Species: *Listeria innocua*  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AD1654  
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ertlan, K.D.; Fsihl, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1654  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1399 <G1A>  
A:Cross-references: GB:ML592022; PIDN:CAC97004.1; PID:g16414260; GSPDB:GN00178  
A:Experimental source: strain C11p11262  
C:Genetics:  
A:Gene: metk  
C:Superfamily: methionine adenosyltransferase

alignment\_scores:  
Quality: 61.00 Length: 18  
Ratio: 4.067 Gaps: 0  
Percent Similarity: 83.333 Percent Identity: 61.111

alignment\_block:

US-09-198-779B-1 x AD1654 ..

Align seg 1/1 to: AD1654 from: 1 to: 399

```

169 AAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGACTTACCTG 218
      ::::::::::::::::::::::::::::::::::::
368 GlnThrAlaAlaPheGlyHisPheGlyArgThrAspValGluLeuProTr 384

219 CGAG 222
      |||
384 pGlu 385

```

seq\_name: p1r2:AH1282

seq\_documentation\_block:

S-methionine adenosyltransferase homolog metk [imported] - *Listeria monocytogenes* (strain C)  
C:Species: *Listeria monocytogenes*  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AH1282

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ertlan, K.D.; Fsihl, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1282  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1399 <G1A>  
A:Cross-references: GB:NC\_003210; PIDN:CAC99742.1; PID:g16411100; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: metk  
C:Superfamily: methionine adenosyltransferase

alignment\_scores:  
Quality: 61.00 Length: 18  
Ratio: 4.067 Gaps: 0  
Percent Similarity: 83.333 Percent Identity: 61.111

alignment\_block:

US-09-198-779B-1 x AH1282 ..

Align seg 1/1 to: AH1282 from: 1 to: 399

```

169 AAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGACTTACCTG 218
      ::::::::::::::::::::::::::::::::::::
368 GlnThrAlaAlaPheGlyHisPheGlyArgThrAspValGluLeuProTr 384

219 CGAG 222
      |||
384 pGlu 385

```

seq\_name: p1r2:F70899

seq\_documentation\_block:

probable metk protein - *Mycobacterium tuberculosis* (strain H37RV)  
C:Species: *Mycobacterium tuberculosis*  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: F70899  
R:Conor, R.; Davies, R.; Parkhill, J.; Garner, T.; Churcher, C.; Harris, D.; Gordon, R.; Rajandream, M.A.; Rogers, J.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome.  
A:Reference number: A70500; MUID:98295987  
A:Accession: F70899  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-403 <COL>  
A:Cross-references: GB:Z80108; GB:AL123456; NID:g3256012; PIDN:CAB02194.1; PID:g32561  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: metk  
C:Superfamily: methionine adenosyltransferase

alignment\_scores:  
Quality: 61.00 Length: 20  
Ratio: 4.067 Gaps: 0  
Percent Similarity: 75.000 Percent Identity: 55.000

alignment\_block:

US-09-198-779B-1 x F70899 ..

Align seg 1/1 to: F70899 from: 1 to: 403

```

163 TTCATCAAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGACTT 212

```

```

::: ||||||||||||||||||||| |||:::
372 TyraAlaProthraAlaAlaTyrGlyHisPheGlyTrpThrSpValGluLe 388
213 CAACTGGAG 222
388 uProTrrpGlu 391
seq_name: p1r2:B97403

```

## seq\_documentation\_block:

```

methionine adenosyltransferase (EC 2.5.1.6) - Agrobacterium tumefaciens (strain C58, Gen
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97403
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194
A:Accession: B97403
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86179.1; PID:g15155274; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_632
A:Map position: circular chromosome
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

```

## alignment\_scores:

```

Quality: 61.00 Length: 30
Ratio: 2.905 Gaps: 2
Percent Similarity: 70.000 Percent Identity: 46.667

```

## alignment\_block:

```

US-09-198-779b-1 x B97403 ..
Align seg 1/1 to: B97403 from: 1 to: 420

```

```

163 TTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGAC.....GA 203
::: |||||||:::|||||||||||||||
384 TyraAlaYthrSerThrSerTyrGlyHisPheGlyTrpThrSpValGluLe 400
204 CGCCGACTTCACCTGGCAG.....GTGGCAAGCCC 234
|:::|||||::: |||
400 pGlySerPheSerTrrpGluLysLeuAspLeuValLysPro 413

```

## seq\_name: p1r2:AB2621

## seq\_documentation\_block:

```

S-adenosylmethionine synthetase metK [imported] - Agrobacterium tumefaciens (strain C58,
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AB2621
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAI41384.1; PID:g17738701; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: metK
A:Map position: circular chromosome

```

## C:Superfamily: methionine adenosyltransferase

```

alignment_scores:
Quality: 61.00 Length: 30
Ratio: 2.905 Gaps: 2
Percent Similarity: 70.000 Percent Identity: 46.667

```

## alignment\_block:

```

US-09-198-779b-1 x AB2621 ..
Align seg 1/1 to: AB2621 from: 1 to: 420

```

```

163 TTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGAC.....GA 203
::: |||||||:::|||||||||||||||
384 TyraAlaYthrSerThrSerTyrGlyHisPheGlyTrpThrSpValGluLe 400
204 CGCCGACTTCACCTGGCAG.....GTGGCAAGCCC 234
|:::|||||::: |||
400 pGlySerPheSerTrrpGluLysLeuAspLeuValLysPro 413

```

## seq\_name: p1r2:AC2211

## seq\_documentation\_block:

```

heme transport protein alr3242 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AC2211
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigun
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2211
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-877 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA874941.1; PID:g17132337; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3242

```

```

alignment_scores:
Quality: 61.00 Length: 36
Ratio: 2.346 Gaps: 0
Percent Similarity: 72.222 Percent Identity: 36.111

```

## alignment\_block:

```

US-09-198-779b-1 x AC2211 ..
Align seg 1/1 to: AC2211 from: 1 to: 877

```

```

12 ACCCTCGGTGGAGACATGACGCTGCGCATGCTGATTAATGACGCTCT 61
||||||| ||| ||| :::
412 SerLeuGlyTyrGlnTyrAspAsnProAsnSerLysSerTrpLeuGlnph 428
62 GATTCATGTTGCTGTTGTTATTAATGTTATTAATGACGACACACA 111
:::|||||::: ||| :::|||||:::|||||
428 eValnArgAlaAsnLeuTyrTyrGlnAsnAlaIleIleGluGluAspSerA 445
112 CACGTACG 119
:::||||:
445 snArgSer 447

```

## seq\_name: p1r2:S74736

## seq\_documentation\_block:

```

methionine adenosyltransferase (EC 2.5.1.6) - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803

```

C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C/Accession: S74736  
R/Keneo, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
s.  
A/Reference number: S74322; MUID:97061201  
A/Accession: S74736  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-409 <KAN>  
A/Cross-references: EMBL:D90901; GB:AE001339; NID:g1651897; PIDN:BAAL6887.1; PID:g165196  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C/Genetics:  
A/Gene: metX  
A/Start codon: GTG  
C/Superfamily: methionine adenosyltransferase  
C/Keywords: S-adenosylmethionine; transferase

alignment\_scores:  
Quality: 60.50 Length: 22  
Ratio: 3.559 Gaps: 1  
Percent Similarity: 77.273 Percent Identity: 59.091

alignment\_block:  
US-09-198-779B-1 x S74736 ..

Align seg 1/1 to: S74736 from: 1 to: 409

160 AGGTCATCAAG...ACCGCGCATACGCGCATTTGGCGTAGACGAC 206  
||||| : : : ||||||| : : : ||||||| : : : |||  
367 ArgPheTYrGlnAspValAlaIleTYrGlnHisPheGlyArgAsnAspLe 383  
207 CGACTTCACCTGCGAG 222  
||||| : : : |||  
383 uAspLeuProTYrGln 388

seq\_name: pir2:E82319

seq\_documentation\_block:  
S-adenosylmethionine synthase VC0472 [imported] - *Vibrio cholerae* (strain N16961 serogroup C)  
C/Species: *Vibrio cholerae*  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C/Accession: E82319  
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;  
Chardson, D.; Ermolaeva, M.D.; Yamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A/Reference number: AB2035; MUID:20406833  
A/Accession: E82319  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-385 <HEI>  
A/Cross-references: GB:AE004133; GB:AE003852; NID:99654889; PIDN:AAF93645.1; GSPDB:GN001  
C/Experimental source: serogroup O1, strain N16961, biotype El Tor  
C/Genetics:  
A/Gene: VC0472  
A/Map position: 1  
C/Superfamily: methionine adenosyltransferase

alignment\_scores:  
Quality: 60.00 Length: 12  
Ratio: 5.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 83.333

alignment\_block:  
US-09-198-779B-1 x E82319 ..

Align seg 1/1 to: E82319 from: 1 to: 385

169 AAGACCGCGCATACGCGCATTTGGCGTAGACGAC 204  
||||| : : : ||||||| : : : ||||||| : : : |||  
355 LysThrAlaAlaTYrGlyHisPheGlyArgGluGlu 366

seq\_name: pir2:B84381

seq\_documentation\_block:  
acylaminoacyl-peptidase [imported] - *Halobacterium* sp. NRC-1  
C/Species: *Halobacterium* sp. NRC-1  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C/Accession: B84381  
R/Ni, W.V.; Kennedy, S.P.; Mahatras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,  
J.; Leithauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; J.  
Jung, K.H.; Alam, M.; Freltas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;  
A/Title: Genome sequence of *Halobacterium* species NRC-1.  
A/Reference number: AB4160; MUID:20504483  
A/Accession: B84381  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-674 <STO>  
A/Cross-references: GB:AE004437; NID:g10581715; PIDN:AAG20414.1; GSPDB:GN00138  
C/Genetics:  
A/Gene: yuxL

alignment\_scores:  
Quality: 60.00 Length: 87  
Ratio: 1.579 Gaps: 3  
Percent Similarity: 43.678 Percent Identity: 28.736

alignment\_block:  
US-09-198-779B-1/rev x B84381 ..

Align seg 1/1 to: B84381 from: 1 to: 674

228 GACCACTCGCGAGTGGCGCTGCGCGCGCAAGCGCGGTATG 179  
||| ||||| : : : ||||| ||||| ||||| ||  
183 AspLeuAlaAlaGlyArgValAspArgValThrAlaGlyValAlaGlu 199  
178 CGCG.....GAACTGNNNNNNNNNNNNNNNNNN 175  
|||  
199 SGlyGlyProAlaTYrGlyAspAspGlyThrLeuTYrTYrProIleArg 216  
174 ..GGTCTTGAT.....GAACTGNNNNNNNNNNNNNNNNNN 142  
||||| ||||| : : : ||||| : : : ||||| : : : |||  
216 rgGlyLeuAspAlaAspAspArgLeuGlyTYrPalaIleGlyAlaIleThr 232  
216 rgGlyLeuAspAlaAspAspArgLeuGlyTYrPalaIleGlyAlaIleThr 232  
141 NNNNNNNNNNNNNNNNNNNNNNAACGTACTGTGTCTCTGCTCAATTATA 92  
::: : : : : : |||  
233 ProAlaAspSerAlaAspSerThrValVal..... 242  
91 CAACATTAATAACACCAACAAATGATCAGACCGCTCATTTATCAGC 42  
||||| : : : ||||| : : : ||||| : : : |||  
243 .....ThrThrValGluGlyMetClyProThrIleuAlaValH 255  
41 ATGGGCGCGGT 31  
||||| : : : |||  
255 ISGlySerArg 258

seq\_name: pir2:A71281

seq\_documentation\_block:  
probable S-adenosylmethionine synthetase (metX) - *Syphilis spirochete*  
C/Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)  
C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 18-Jun-1999  
C/Accession: A71281  
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.;  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.;  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998

```
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770
A:Accession: A71281
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-396 <COL>
A:Cross-references: GB:AE001250; GB:AE000520; NID:93323096; PIDN:AA65758.1; PID:9332310
C:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0794
C:Superfamily: methionine adenosyltransferase

alignment_scores:
  Quality: 59.00      Length: 33
  Ratio: 2.565      Gaps: 2
  Percent Similarity: 69.697      Percent Identity: 39.394

alignment_block:
  US-09-198-779B-1 x A71281  ..

Align seg 1/1 to: A71281 from: 1 to: 396

160 AGCTTCATCAAGACCGCGCATACGCCACTTGGCCGTCAGCAGC..... 204
||||: |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
355 ArgTyrArgSerThrAlaValTyrGlyHisPheGlyArgGluGlnPhePr 371
205 .....GCCGACTTCACCTGCGAGGTG.....GTCAAGCC 234
||||: |||:|||||:|||||:|||||:|||||:|||||:|||||:
371 OTTGTGTAArgThrAspCysValCysAspLeuGlnArgAlaValArgPro 387

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - mouse
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-May-2000
R:Sakata, S.F.; Shelly, L.L.; Ruppert, S.; Schutz, G.; Chou, J.Y.
J. Biol. Chem. 268, 13978-13986, 1993
A:Title: Cloning and expression of murine S-adenosylmethionine synthetase.
A:Reference number: A47151; MUID:93300783
A:Accession: A47151
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-396 <SAK>
A:Experimental source: liver
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:134412, NCBIIP:134413)
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
  Quality: 59.00      Length: 21
  Ratio: 3.688      Gaps: 1
  Percent Similarity: 76.190      Percent Identity: 61.905

alignment_block:
  US-09-198-779B-1 x A47151  ..

Align seg 1/1 to: A47151 from: 1 to: 396

169 AAGACCGCGCATACGCCACTTGGCCGTCAGCAGCCGACTTCACCTG 218
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
374 LysThrAlaCysTyrGlyHisPheGlyArg.....SerGluPheProTr 388
219 CGAGGTGTCAG 231
||||| |||
388 pGluValProLys 392

seq_name: plr2:S06114

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - rat
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-May-2000
R:Horikawa, S.; Ishikawa, M.; Ozasa, H.; Tsukada, K.
Eur. J. Biochem. 184, 497-501, 1989
A:Title: Isolation of a cDNA encoding the rat liver S-adenosylmethionine synthetase.
A:Reference number: S06114; MUID:90032633
A:Accession: S06114
A:Molecule type: mRNA
A:Residues: 1-397 <HOR>
A:Cross-references: EMBL:X15734; NID:957183; PIDN:CAA33754.1; PID:957184
R:Mato, J.M.
submitted to the EMBL Data Library, July 1991
A:Reference number: S18256
A:Accession: S18256
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-397 <MAT>
A:Cross-references: EMBL:X60822
R:Alvarez, L.; Asuncion, M.; Corrales, F.; Pajares, M.A.; Mato, J.M.
FEBS Lett. 290, 142-146, 1991
A:Title: Analysis of the 5' non-coding region of rat liver S-adenosylmethionine synth
A:Reference number: S18257; MUID:92008649
A:Accession: S18257
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-46 <ALV>
A:Cross-references: EMBL:X60822
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
  Quality: 59.00      Length: 21
  Ratio: 3.688      Gaps: 1
  Percent Similarity: 76.190      Percent Identity: 61.905

alignment_block:
  US-09-198-779B-1 x S06114  ..

Align seg 1/1 to: S06114 from: 1 to: 397

169 AAGACCGCGCATACGCCACTTGGCCGTCAGCAGCCGACTTCACCTG 218
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
375 LysThrAlaCysTyrGlyHisPheGlyArg.....SerGluPheProTr 389
219 CGAGGTGTCAG 231
||||| |||
389 pGluValProLys 393
```

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|||||  
40 pperhrrtprgluValValysPro 48

seq\_name: sp\_plant:Q944U4

seq\_documentation\_block:  
ID Q944U4 PRELIMINARY; PRT; 395 AA.  
AC Q944U4;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE S-ADENOSYL-L-METHIONINE SYNTHETASE.  
GN SAMS.  
OS Dendrobium crumenatum (Tropical pigeon orchid).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendrobilinae;  
OC Dendrobium.  
OX NCBI\_Taxid=51096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Han P., Pua E.C.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF20238; AAL16064.1;  
SQ SEQUENCE 395 AA; 43210 MW; 240AA4A7CF8DA440 CRC64;

alignment\_scores:  
Quality: 122.00 Length: 25  
Ratio: 5.304 Gaps: 0  
Percent Similarity: 92.000 Percent Identity: 92.000

alignment\_block:

US-09-198-779b-1 x Q944U4 ..

Align seg 1/1 to: Q944U4 from: 1 to: 395

160 AGGTCATCATAGAGCCGCCATACGCGCATTGGCCGTGACGAGCCGA 209  
|||||  
363 ArgpHeuLeuYstHrAlaIatYrgLHsPheGlyArgAspAspThrAs 379  
210 CTTCACCTGCGAGGTGTCACGCC 234  
|||||  
379 pperhrrtprgluValValysPro 387

seq\_name: sp\_plant:Q94C00

seq\_documentation\_block:  
ID Q94C00 PRELIMINARY; PRT; 80 AA.  
AC Q94C00;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE S-ADENOSYL METHIONINE SYNTHETASE (FRAGMENT).  
GN SAMS1.  
OS Elaeis oleifera.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoidae;  
OC Cocoeae; Elaeidinae; Elaeis.  
OX NCBI\_Taxid=80265;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bhore S.J., Shah F.H.;  
RL "Isolation of S-adenosyl-L-methionine synthetase (SAMS1) cDNA clone  
from oil palm (Elaeis oleifera) mesocarp tissue."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY039010; AAK72126.1;  
FT NON\_TER 1  
SQ SEQUENCE 80 AA; 8983 MW; B1F012583F825776 CRC64;

alignment\_scores:  
Quality: 121.00 Length: 25

Ratio: 5.042 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779b-1 x Q94C00 ..

Align seg 1/1 to: Q94C00 from: 1 to: 80

160 AGGTCATCATAGAGCCGCCATACGCGCATTGGCCGTGACGAGCCGA 209  
|||||  
48 ArgpHeuLeuYstHrAlaIatYrgLHsPheGlyArgAspAspThrAs 64  
210 CTTCACCTGCGAGGTGTCACGCC 234  
|||||  
64 pperhrrtprgluValValysPro 72

seq\_name: sp\_plant:Q9SBQ7

seq\_documentation\_block:  
ID Q9SBQ7 PRELIMINARY; PRT; 393 AA.  
AC Q9SBQ7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).  
OS Petunia hybrida (Petunia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
OX NCBI\_Taxid=4102;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. VIOLET; TISSUE=COROLLA;  
RX MEDLINE=20027448; PubMed=10557255;  
RA Soong S.C., To K.Y.;  
RT "Nucleotide sequence of A cDNA (AF170798) Encoding Type I S-  
adenosyl-L-methionine Synthetase from Petunia hybrida. (PGR99-160).";  
RL Plant Physiol. 121:1053-1053(1999).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
METHIONINE AND ATP (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.  
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
DR EMBL; AF170798; AAD48485.1; ..  
DR HSSP; P04384; 1MB.  
DR InterPro; IPR002133; S-Adomet\_synth.  
DR Pfam; PF00438; S-Adomet\_synth. 1.  
DR Pfam; PF02772; S-Adomet\_synth2; 1.  
DR Pfam; PF02773; S-Adomet\_synth3; 1.  
DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_1; 1.  
DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
KW ATP-binding; One-carbon metabolism; Transferrase.  
SQ SEQUENCE 393 AA; 43169 MW; 0AC0DD62F28F6749 CRC64;

alignment\_scores:  
Quality: 121.00 Length: 25  
Ratio: 5.042 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779b-1 x Q9SBQ7 ..

Align seg 1/1 to: Q9SBQ7 from: 1 to: 393

160 AGGTCATCATAGAGCCGCCATACGCGCATTGGCCGTGACGAGCCGA 209  
|||||  
361 ArgpHeuLeuYstHrAlaIatYrgLHsPheGlyArgAspAspThrAs 377  
210 CTTCACCTGCGAGGTGTCACGCC 234  
|||||

377 pphenhrtrpgluvalvalyspro 385

seq\_name: sp\_plant:Q9S992

seq\_documentation\_block:

ID Q9S992 PRELIMINARY; PRT: 68 AA.

AC Q9S992;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MET ADENOSYLTRANSFERASE HOMOLOG (FRAGMENT).  
 OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 NCBI\_TaxID=3708;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94302145; PubMed=8029332;  
 RA Park Y.S., Kwak J.M., Kwon O.Y., Kim Y.S., Lee D.S., Cho M.J.,  
 RA Lee H.H., Nam H.G.;  
 RT "Generation of expressed sequence tags of random root cDNA clones of  
 RL Brassica napus by single-run partial sequencing.";  
 RL Plant Physiol. 103:359-370(1993).  
 DR HSSP: P04384; IMXB.  
 DR InterPro: IPR002133; S-Adomet\_synth.  
 DR Pfam: PF00438; S-Adomet\_synth; 1.  
 DR Pfam: PF02773; S-Adomet\_synth2; 1.  
 SO SEQUENCE 68 AA; 7836 MW; B806D7D3E7589763 CRC64;

alignment\_scores:

Quality:	120.00	Length:	25
Ratio:	5.217	Gaps:	0
Percent Similarity:	92.000	Percent Identity:	88.000

alignment\_block:

US-09-198-779B-1 x Q9S992 ..

Align seg 1/1 to: Q9S992 from: 1 to: 68

160 AGGTTTCATCAAGAGCCGCCATACGCCATTGGCGTGACGAGCCGA 209  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||  
 36 ArgPheLeuLysThrAlaIatryGlyHisPheGlyArgAspAspProAs 52  
 210 CTTCACTGCGAGGTGTCAGAGCC 234  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 52 pphenhrtrpgluvalvalyspro 60

seq\_name: sp\_plant:Q941A8

seq\_documentation\_block:

ID Q941A8 PRELIMINARY; PRT: 368 AA.

AC Q941A8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE AT1G02500/T14P4\_22.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,  
 RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,  
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,  
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

RT "Arabidopsis cDNA clones.";  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY052311; AAK96504.1; -  
 SO SEQUENCE 368 AA; 40471 MW; EF440A6C4B3D2054 CRC64;

alignment_scores:	Quality:	120.00	Length:	25
Ratio:	5.217	Gaps:	0	
Percent Similarity:	92.000	Percent Identity:	88.000	

alignment\_block:

US-09-198-779B-1 x Q941A8 ..

Align seg 1/1 to: Q941A8 from: 1 to: 368

160 AGGTTTCATCAAGAGCCGCCATACGCCATTGGCGTGACGAGCCGA 209  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||  
 336 ArgPheLeuLysThrAlaIatryGlyHisPheGlyArgAspAspProAs 352  
 352 pphenhrtrpgluvalvalyspro 360

seq\_name: sp\_plant:Q9FEE0

seq\_documentation\_block:

ID Q9FEE0 PRELIMINARY; PRT: 393 AA.

AC Q9FEE0;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE T14P4.17 (S-ADENOSYLMETHIONINE SYNTHETASE) (AT1G02500/T14P4\_22).  
 GN T14P4.17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,  
 RA Ecker J.;  
 RT "Full length cDNA sequence of Arabidopsis thaliana.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,  
 RA Altati H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,  
 RA Buehler E., Chao Q., Chin C., Chlou J., Choi E., Gonzalez A.,  
 RA Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,  
 RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,  
 RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RT "Arabidopsis cDNA clones.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF325061; AAG40413.1; -  
 DR EMBL: AC022521; AAG10639.1; -  
 DR EMBL: AF428440; AAL16209.1; -  
 DR HSSP: P04384; IMXB.  
 DR InterPro: IPR002133; S-Adomet\_synth.  
 DR Pfam: PF00438; S-Adomet\_synth; 1.  
 DR Pfam: PF02772; S-Adomet\_synth2; 1.

DR Pfam: PF02773; S-Adomet\_synth3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE.1; 1.  
 SQ SEQUENCE 393 AA; 43158 MW; 27B0AF8AF55D2PF3 CRC64;

alignment\_scores:  
 Quality: 120.00 Length: 25  
 Ratio: 5.217 Gaps: 0  
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:  
 US-09-198-779B-1 x Q9FEEO ..

Align seg 1/1 to: Q9FEEO from: 1 to: 393

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160 AGGTCATCAAGACCGCGCATAGCGCCACTTGCGCGTGCAGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 ArgPheLeuYstInAlaAlaItyrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACTGCGAGGTGTCAGACCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 PheThrTrpGluValValysPro 385

```

seq\_name: sp\_plant:Q94FA6

seq\_documentation\_block:  
 ID Q94FA6 PRELIMINARY; PRT; 393 AA.

AC Q94FA6:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE S-ADENOSYLMETHIONINE SYNTHETASE.  
 GN MSAMS.  
 OS Brassica juncea (leaf mustard) (Indian mustard).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pua E.C., Lim C.C., Liu J.Z.;  
 RT "Molecular cloning of S-adenosylmethionine genes from mustard.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF379013; AAK71233.1; -  
 SQ SEQUENCE 393 AA; 43141 MW; E7598AC6BD4A0DE CRC64;

alignment\_scores:  
 Quality: 120.00 Length: 25  
 Ratio: 5.217 Gaps: 0  
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:  
 US-09-198-779B-1 x Q94FA6 ..

Align seg 1/1 to: Q94FA6 from: 1 to: 393

```

160 AGGTCATCAAGACCGCGCATAGCGCCACTTGCGCGTGCAGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 ArgPheLeuYstInAlaAlaItyrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACTGCGAGGTGTCAGACCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 PheThrTrpGluValValysPro 385

```

seq\_name: sp\_plant:Q94FA4

seq\_documentation\_block:  
 ID Q94FA4 PRELIMINARY; PRT; 393 AA.

AC Q94FA4:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE.2; 1.  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE S-ADENOSYLMETHIONINE SYNTHETASE.

GN MSAMS.

OS Brassica juncea (leaf mustard) (Indian mustard).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Brassica.

OX NCBI\_TaxID=3707;

RN [1]

RP SEQUENCE FROM N.A.

RA Pua E.C., Lim C.C., Liu J.Z.;

RT "Molecular cloning of S-adenosylmethionine genes from mustard.";

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF379015; AAK71235.1; -

SQ SEQUENCE 393 AA; 43184 MW; 4E5019EDDF28DA7 CRC64;

alignment\_scores:  
 Quality: 120.00 Length: 25  
 Ratio: 5.217 Gaps: 0  
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment\_block:  
 US-09-198-779B-1 x Q94FA4 ..

Align seg 1/1 to: Q94FA4 from: 1 to: 393

```

160 AGGTCATCAAGACCGCGCATAGCGCCACTTGCGCGTGCAGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 ArgPheLeuYstInAlaAlaItyrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACTGCGAGGTGTCAGACCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 PheThrTrpGluValValysPro 385

```

seq\_name: sp\_plant:Q9AT55

seq\_documentation\_block:  
 ID Q9AT55 PRELIMINARY; PRT; 393 AA.

AC Q9AT55:  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).  
 GN SAMS2.  
 OS Elaeagnus umbellata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Elaeagnaceae; Elaeagnus.  
 OX NCBI\_TaxID=43233;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lee S., An C.;  
 RT "Structures and expression patterns of two cDNA clones encoding S-  
 RT adenosyl-L-methionine synthetase from the root module of Elaeagnus  
 RT umbellata".  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 CC METHIONINE AND ATP (BT SIMILARITY).  
 CC -I- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
 CC PYROPHOSPHATE + S'-ADENOSYL-L-METHIONINE.  
 CC -I- PATHWAY: ACTIVATED METHYL CYCLE.  
 CC -I- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 DR EMBL; AF346306; AAK29410.1; -  
 DR HSSP; P04384; IMXB.  
 DR InterPro; IPR002133; S-Adomet\_synth.  
 DR Pfam; PF00438; S-Adomet\_synth.1.  
 DR Pfam; PF02772; S-Adomet\_synth2; 1.  
 DR Pfam; PF02773; S-Adomet\_synth3; 1.  
 DR PROSITE; PS00376; ADOMET\_SYNTHETASE.1; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE.2; 1.  
 KW ATP-binding; One-carbon metabolism; Transferrase.



377 pphethrtrpgluvallylpspro 385

seq\_name: sp\_plant:Q9AT56

seq\_documentation\_block: PRELIMINARY; PRT; 393 AA.

AC Q9AT56;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
 DE ADENOSYLTTRANSFERASE) (ADOMET SYNTHETASE).  
 GN SAM51.  
 OS Eleagnus umbellata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Elaeagnaceae; Elaeagnus.  
 OX NCBI\_TaxID=43233;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ROOT MODULE:  
 RA Lee S., An C.;  
 RT "Structures and expression patterns of two cDNA clones encoding S-  
 RT adenosyl-L-methionine synthetase from the root module of Elaeagnus  
 RT umbellata.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 CC METHIONINE AND ATP (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
 CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.  
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 DR EMBL: AF346305; AAK29409.1; -  
 DR HSSP: P04384; IMXB.  
 DR InterPro: IPR002133; S-Adomet\_synt.  
 DR Pfam: PF00438; S-Adomet\_synt2; 1.  
 DR Pfam: PF02772; S-Adomet\_syntD2; 1.  
 DR Pfam: PF02773; S-Adomet\_syntD3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; One-carbon metabolism; Transferrase.  
 SQ SEQUENCE 393 AA; 43097 MW; E6DFPD2A9FAD2347 CRC64;

alignment\_scores:

Quality:	115.00	Length:	25
Ratio:	5.000	Gaps:	0
Percent Similarity:	92.000	Percent Identity:	80.000

alignment\_block:

US-09-198-779B-1 x Q9AT56 ..

Align seg 1/1 to: Q9AT56 from: 1 to: 393

160 AGGTTTCATCAGACCGCCGATACGCGCATTTGGCCGTGACGACGCCGA 209  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||  
 361 Argphelaulysthralalaglytytycylhisphneglyargaspasproas 377  
 210 CTTCACCTGCGAGGTGTCACGCC 234  
 ||||| |||||:|||||:|||||  
 377 pphethrtrpgluvallylpspro 385

seq\_name: sp\_plant:Q94FA5

seq\_documentation\_block: PRELIMINARY; PRT; 390 AA.

AC Q94FA5;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE S-ADENOSYLMETHIONINE SYNTHETASE.  
 GN MSAMS.  
 OS Brassica juncea (Leaf mustard) (Indian mustard).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pua E.C., Lim C.C., Liu J.Z.;  
 RT "Molecular cloning of S-adenosylmethionine genes from mustard.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF379014; AAK71234.1; -  
 SQ SEQUENCE 390 AA; 42599 MW; DC4A25C72CC25322 CRC64;

alignment\_scores:

Quality:	114.00	Length:	25
Ratio:	5.182	Gaps:	0
Percent Similarity:	86.000	Percent Identity:	84.000

alignment\_block:

US-09-198-779B-1 x Q94FA5 ..

Align seg 1/1 to: Q94FA5 from: 1 to: 390

160 AGGTTTCATCAGACCGCCGATACGCGCATTTGGCCGTGACGACGCCGA 209  
 ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:||  
 361 Argphelaulysthralalaglytytycylhisphneglyargaspasproas 377  
 210 CTTCACCTGCGAGGTGTCACGCC 234  
 ||||| |||||:|||||:|||||  
 377 pphethrtrpgluvallylpspro 385

seq\_name: sp\_plant:Q9LG06

seq\_documentation\_block: PRELIMINARY; PRT; 396 AA.

AC Q9LG06;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
 DE ADENOSYLTTRANSFERASE) (ADOMET SYNTHETASE).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Pharbitidae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RC Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone: p0706805.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 CC METHIONINE AND ATP (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
 CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.  
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 DR EMBL: AP002482; BAA96637.1; -  
 DR HSSP: P04384; IMXB.  
 DR InterPro: IPR002133; S-Adomet\_synt.  
 DR Pfam: PF00438; S-Adomet\_synt; 1.  
 DR Pfam: PF02772; S-Adomet\_syntD2; 1.  
 DR Pfam: PF02773; S-Adomet\_syntD3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; One-carbon metabolism; Transferrase.  
 SQ SEQUENCE 396 AA; 43310 MW; A56C239B8389CC5D1 CRC64;

alignment\_scores:

Quality:	113.00	Length:	25
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Ratio: 4.913  
Percent Similarity: 92.000 Percent Identity: 80.000

alignment\_block:  
US-09-198-779b-1 x Q9L6U6 ..

Align seg 1/1 to: Q9L6U6 from: 1 to: 396

```

160 AGGTTATCATGACGCCGATACGCCACTTGGCCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
364 ArgTyrluEuSthrAlaAlaTyrGlyHisPheGlyArgGlnAspProAs 380
210 CTCACCTCGAGGTGTGTCAGCC 234
||||| ||||||| ||||||| ||||||| ||
380 pphenThrTrpGluValValysPro 388

```

seq\_name: sp\_plant:Q9FVG7

seq\_documentation\_block:

```

ID Q9FVG7 PRELIMINARY; PRT; 393 AA.
AC Q9FVG7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6).
GN SAMS2.
OS Pinus contorta (Shore pine) (Lodgepole pine).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=33319;
RN [1]
RP MEDLINE=21380671; PubMed=11488480;
RX Lindroth A.M., Saarikoski P., Flyvén G., Clapham D., Gronroos R.,
RA Thelander M., Rönne H., von Arnold S.;
RT "Two S-adenosylmethionine synthetase-encoding genes differentially
RT expressed during adventitious root development in Pinus contorta.";
RL Plant Mol. Biol. 46:335-346(2001).
DR EMBL: AF187821; AAG17036.1;
DR HSSP: P04384; IMXB;
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
KW Transferase
SO SEQUENCE 393 AA; 43068 MW; 5824C18313820F30 CRC64;

```

alignment\_scores:

Quality: 111.00 Length: 25  
Ratio: 5.045 Gaps: 0  
Percent Similarity: 88.000 Percent Identity: 84.000

alignment\_block:  
US-09-198-779b-1 x Q9FVG7 ..

Align seg 1/1 to: Q9FVG7 from: 1 to: 393

```

160 AGGTTATCATGACGCCGATACGCCACTTGGCCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgPheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377
210 CTCACCTCGAGGTGTGTCAGCC 234
||||| ||||||| ||||||| ||||||| ||
377 pphenThrTrpGluThrValysPro 385

```

seq\_name: sp\_plant:Q9FPL6

seq\_documentation\_block:

```

ID Q9FPL6 PRELIMINARY; PRT; 395 AA.
AC Q9FPL6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)

```

```

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE 2.
OS Sueda maritima subsp. salsa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Sueda.
OX NCBI_TaxID=126914;
RN [1]
RP SEQUENCE FROM N.A.
RL Ma X., Zhang H.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321001; AAC42490.1;
DR HSSP: P04384; IMXB;
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_2; 1.
SO SEQUENCE 395 AA; 43008 MW; 8901451D723988D8 CRC64;

```

alignment\_scores:

Quality: 111.00 Length: 25  
Ratio: 5.045 Gaps: 0  
Percent Similarity: 88.000 Percent Identity: 84.000

alignment\_block:  
US-09-198-779b-1 x Q9FPL6 ..

Align seg 1/1 to: Q9FPL6 from: 1 to: 395

```

160 AGGTTATCATGACGCCGATACGCCACTTGGCCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgPheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377
210 CTCACCTCGAGGTGTGTCAGCC 234
||||| ||||||| ||||||| ||||||| ||
377 pphenThrTrpGluThrValysPro 385

```

seq\_name: sp\_plant:O22350

seq\_documentation\_block:

```

ID O22350 PRELIMINARY; PRT; 179 AA.
AC O22350;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (FRAGMENT).
GN CHRSAMS.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RL STRAIN=137C;
RL Kim J.Y., Lee K.O., Lee S.H.;
RT "Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF008568; AAB71853.1;
DR HSSP: P04384; IMXB;
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR NON_TER 1
DT SEQUENCE 179 AA; 19459 MW; 76559D3B5C0E78B5 CRC64;

```

alignment\_scores:

Quality: 101.00 Length: 24

Ratio: 4.810 Gaps: 0  
Percent Similarity: 87.500 Percent Identity: 79.167

## alignment\_block:

US-09-198-779B-1 x 022350 ..

Align seg 1/1 to: 022350 from: 1 to: 179

160 AGGTTTCATCAGACCGCGCATACGGCCATTGGCCGTGAGACGCCGA 209  
|||||  
153 ArglyrglnLysThrAlaAlaIArgLysHisPheGlyArgAspAspProAs 169  
210 CTTCACTGCGAGGTGTCTAAG 231  
|||||  
169 pPheThrTrpGluThrValLys 176

## seq\_name: sp\_Plant:Q9SBQ5

## seq\_documentation\_block:

ID Q9SBQ5 PRELIMINARY; PRT; 390 AA.  
AC Q9SBQ5;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).  
GN SAM2.  
OS Petunia hybrida (Petunia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
OX NCBI\_TaxID=4102;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VIOLET; TISSUE=COROLLA;  
RX PubMed=10759541;  
RA Hsu Y.H., To K.Y.;  
RT "Cloning of a cDNA (accession no. AF183891) encoding type II S-adenosyl-L-methionine synthetase from Petunia (PGR00-033).";  
RL Plant Physiol. 122:1457-1457(2000).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
CC METHIONINE AND ATP (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.  
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
DR EMBL: AF183891; AAD56396.1; -.  
DR HSSP: P04384; IMXB.  
DR InterPro: IPR002133; S-Adomet\_synt.  
DR Pfam: PF00438; S-Adomet\_syntd2; 1.  
DR Pfam: PF02772; S-Adomet\_syntd3; 1.  
DR Pfam: PF02773; S-Adomet\_syntd3; 1.  
DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
KW ATP-binding; One-carbon metabolism; Transferase.  
SQ SEQUENCE 390 AA; 42593 MW; D46F4618732CA31 CRC64;

## alignment\_scores:

Quality: 101.00 Length: 24  
Ratio: 4.810 Gaps: 0  
Percent Similarity: 87.500 Percent Identity: 79.167

## alignment\_block:

US-09-198-779B-1 x Q9SBQ5 ..

Align seg 1/1 to: Q9SBQ5 from: 1 to: 390

160 AGGTTTCATCAGACCGCGCATACGGCCATTGGCCGTGAGACGCCGA 209  
|||||  
361 ArglyrglnLysThrAlaAlaIArgLysHisPheGlyArgAspAspProAs 377  
210 CTTCACTGCGAGGTGTCTAAG 231

|||||  
377 pPheThrTrpGluThrValLys 384

## seq\_name: sp\_Plant:Q9LDQ7

## seq\_documentation\_block:

ID Q9LDQ7 PRELIMINARY; PRT; 393 AA.  
AC Q9LDQ7;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).  
GN SAM.  
OS Camellia sinensis (Tea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; Ericales; Theaceae; Camellia.  
OX NCBI\_TaxID=4442;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Feng Y.F., Liang Y.R.;  
RT "Cloning of s-adenosylmethionine synthetase gene in tea plant.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LEAF;  
RA Feng Y.F., Liang Y.R.;  
RT "s-adenosylmethionine synthetase gene.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
CC METHIONINE AND ATP (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.  
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
DR EMBL: AJ277206; CAB83039.1; -.  
DR EMBL: AB041534; BAA94605.1; -.  
DR HSSP: P04384; IMXB.  
DR InterPro: IPR002133; S-Adomet\_synt.  
DR Pfam: PF00438; S-Adomet\_synt; 1.  
DR Pfam: PF02772; S-Adomet\_syntd2; 1.  
DR Pfam: PF02773; S-Adomet\_syntd3; 1.  
DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
KW ATP-binding; One-carbon metabolism; Transferase.  
SQ SEQUENCE 393 AA; 42800 MW; 67F3D2C50DA42682 CRC64;

## alignment\_scores:

Quality: 100.00 Length: 21  
Ratio: 5.263 Gaps: 0  
Percent Similarity: 90.476 Percent Identity: 85.714

## alignment\_block:

US-09-198-779B-1 x Q9LDQ7 ..

Align seg 1/1 to: Q9LDQ7 from: 1 to: 393

160 AGGTTTCATCAGACCGCGCATACGGCCATTGGCCGTGAGACGCCGA 209  
|||||  
361 ArgPheLeuLysThrAlaAlaIArgLysHisPheGlyArgAspAspProAs 377  
210 CTTCACTGCGAG 222  
|||||  
377 pPheThrTrpGlu 381

## seq\_name: sp\_Plant:Q9M7K8

## seq\_documentation\_block:

ID Q9M7K8 PRELIMINARY; PRT; 390 AA.  
AC Q9M7K8;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)





CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.

DR EMBL; AL159139; CAB76898.1; -

seq\_name: sp\_bacteria:Q9K5E4

	seq_documentation_block:
ID	098A80
PRELIMINARY:	PRT; 391 AA.
AC	098A80;
DT	01-OCT-2001 (TREMblrel, 18, Created)
DT	01-OCT-2001 (TREMblrel, 18, last sequence update)
DT	01-OCT-2001 (TREMblrel, 18, last annotation update)
DE	S-AENOSYLMETHIONINE SYNTHETASE.
MLR615.	
OS	Rhizobium loti (Mesorhizobium loti).
OS	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group

OC phylobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Kochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti.";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL: AP003008; BAB52457.1;  
 DR InterPro: IPR002133; S-Adomet\_synt.  
 DR Pfam: PF00438; S-Adomet\_synt; 1.  
 DR Pfam: PF02772; S-Adomet\_synt2; 1.  
 DR Pfam: PF02773; S-Adomet\_synt3; 1.  
 KW Complete proteome.  
 SO SEQUENCE 391 AA; 42195 MW; 099E0643FE1B086D CRC64;

alignment\_scores:  
 Quality: 66.00 Length: 17  
 Ratio: 4.400 Gaps: 0  
 Percent Similarity: 88.235 Percent Identity: 64.706

alignment\_block:  
 us-09-198-779b-1 x Q98A80 ..

Align seg 1/1 to: Q98A80 from: 1 to: 391

```

172 ACCGCCGATACGCCACTTGGCCGTGACGACGCCGACTTACCTGCGA 221
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
358 ThrAlaThrTyrGlyHisPheGlyArgGluGlnProGluPheThrIrp61 374
222 G 222
374 u 374

```

seq\_name: sp\_bacteriap:Q9AC18

seq\_documentation\_block:  
 ID Q9AC18 PRELIMINARY; PRT; 407 AA.  
 AC Q9AC18;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).  
 GN METK OR CC0050.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
 OC Caulobacter.  
 OX NCBI\_TaxID=69394;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=11259647;  
 RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA DeBoy R.T., Dodson R.D., Durkin A.S., Gwinn M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
 RA Urdaneta J., Tran J., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 CC METHIONINE AND ATP (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
 CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.

CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 DR EMBL: AE005679; AAK22038.1;  
 DR HSSP: P04384; IMXB.  
 DR TIGR: CC0050;  
 DR InterPro: IPR002133; S-Adomet\_synt.  
 DR Pfam: PF00438; S-Adomet\_synt; 1.  
 DR Pfam: PF02772; S-Adomet\_synt2; 1.  
 DR Pfam: PF02773; S-Adomet\_synt3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW AMP-binding; Complete proteome; One-carbon metabolism; Transferase.  
 SO SEQUENCE 407 AA; 43818 MW; E640BC115435FD92 CRC64;

alignment\_scores:  
 Quality: 64.50 Length: 72  
 Ratio: 1.792 Gaps: 3  
 Percent Similarity: 50.000 Percent Identity: 27.778

alignment\_block:  
 us-09-198-779b-1 x Q9AC18 ..

Align seg 1/1 to: Q9AC18 from: 1 to: 407

```

16 TCGGTGGACAGATCGACGCTGCCATGCTGATTAATGACGCTCCTGATC 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
344 AlaValLeuGluLysThrLeuProGlnLeuIleGlyGlyAlaThrProAr 360
66 CATGTGTGCTGTGTTATTAATGTTATTAATGAGCAGACAGACAAACAGC 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
360 galAlaIleArg.....GluHisL 366
116 TAGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
366 euGlnLeuAsnArgProIle.....Tyr 373
166 ATCAGACGCCGCGCATACGCCGCTTGGCCGT.....GAGCAGCC 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
374 AlaArgThrAlaAlaIleTyrGlyHisPheGlyArgThrProAspAsnGlu 390
207 CGACTTCACCTCGCAG 222
: |||||: |||
390 yGlyPheSerTrpGlu 395

```

seq\_name: sp\_bacteriap:Q9P077

seq\_documentation\_block:  
 ID Q9P077 PRELIMINARY; PRT; 376 AA.  
 AC Q9P077;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE  
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).  
 GN METK OR U0412.  
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=134821;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SEVOVAR 3;  
 RX MEDLINE=20500219; PubMed=11048724;  
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 RA Cassell G.H.;  
 RT "The complete sequence of the mucosal pathogen ureaplasma  
 urealyticum.";  
 RL Nature 407:757-762(2000).  
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 CC METHIONINE AND ATP (BY SIMILARITY).

Quality:	64.00	Length:	30
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1415 rogluGlyAsnSerGluHisSerGlySerSerAspSer..... 142

```

111 TTGTGCTCCGCAATTATACACATTAATACACACACACATGATC 62
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1428 LeutppluAlaSerleuGluAsnValSerGlyThrHisPAlaProAl 1444
    ::||| ||||| ::||| |||||
1444 AlaProSerValAlaIleGlnValSerArgSerMetValHisGln 1459
seq_name: sp_rodent:Q99J57

seq_documentation_block:
ID   Q99J57          PRELIMINARY;          PRT;          395 AA.
AC   Q99J57;
DT   01-JUN-2001 (Tremblrel. 17, Created)
DT   01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE   PUTATIVE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
DE   ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC   -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC   METHIONINE AND ATP (BY SIMILARITY).
CC   -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC   PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC   -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC   -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
DR   EMBL: BC003451; AAH03451.1; -.
DR   HSSP: P04384; 1MXB.
DR   InterPro: IPR002133; S-Adomet_synth.
DR   Pfam: PF00438; S-Adomet_synth; 1.
DR   Pfam: PF02772; S-Adomet_synth2; 1.
DR   Pfam: PF02773; S-Adomet_synth3; 1.
DR   PROSITE: PS00377; ADOMET_SYNTHETASE_1; 1.
DR   PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW   ATP-binding; Hypothetical protein; One-carbon metabolism; Transferase.
SQ   SEQUENCE 395 AA; 4368 MW; BB977989B75CB8F9 CRC64;

alignment_scores:
Quality: 63.00 Length: 21
Ratio: 3.938 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 66.667

alignment_block:
US-09-198-779B-1 x Q99J57  ..

Align seg 1/1 to: Q99J57 from: 1 to: 395

169 AAGACGGCGCATACGGCCACTTTGGCGGTGACGACGGCGGACATTCACCTG 218
    ::||| ||||| ||||| ||||| ||||| ||||| |||||
373 ArgThrAlaAlaIleTyrGlyHisPheGlyArgAsp.....SerPheProTr 387
219 CGAGGTGCTCAAG 231
    ||||| |||
387 pGluValProLys 391.

seq_name: sp_bacteriap:Q9A718

seq_documentation_block:
ID   Q9A718          PRELIMINARY;          PRT;          589 AA.
AC   Q9A718;
DT   01-JUN-2001 (Tremblrel. 17, Created)
DT   01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT   01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN CC1908.
DE   CC1908.
GN

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OS   Caulobacter crescentus.
OC   Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC   Caulobacter
OX   NCBI_TaxID=69394;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 19089 / CB15;
RX   MEDLINE=21173698; Pubmed=11259647;
RA   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA   Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA   Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA   DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA   Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry R.,
RA   Uitterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA   Salzberg S.L., Venter J.C., Shapiro I., Fraser C.M.;
RT   "Complete genome sequence of Caulobacter crescentus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR   EMBL: AE005864; AAK3883.1; -.
DR   TIGR: CC1908; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE 589 AA; 59269 MW; A7E52050C891B98A CRC64;

alignment_scores:
Quality: 63.00 Length: 61
Ratio: 1.909 Gaps: 2
Percent Similarity: 54.098 Percent Identity: 31.148

alignment_block:
US-09-198-779B-1 x Q9A718  ..

Align seg 1/1 to: Q9A718 from: 1 to: 589

53 GACGCTCCGTCACATTCGTTGCTGCTGTATTAATGTTATATTGAGC 102
    ||||| ||||| |||||
240 AspGlyProAspPro.....G1 245
103 AGACACACACACAGTACGTTGTTNNNNNNNNNNNNNNNNNNNNNNNN 152
    ||| ||||| ::||| ::||| ::||| ::||| ::||| ::|||
245 nGlyProMetThrHisGlnAlaArgAlaAsnGlySerSerSerAlaG 262
153 NNNNNNACGGTTCATCAAGACCGCCGATACGGCCACTTTGGCGGTGACG 202
    ::||| ||||| ||||| ||||| ||||| |||||
262 lYAlaMetAlaSerSer...ProProAlaGlnSerArgGluAlaAlaAsp 277
203 ACGCGGACTTCACCTCGCGAGGTGTCACGCCCC 235
    ::||| ::||| ||||| ||||| |||||
278 AlaProAspAlaProAlaAlaThrSerPro 288

seq_name: sp_bacteriap:Q98PMO

seq_documentation_block:
ID   Q98PMO          PRELIMINARY;          PRT;          376 AA.
AC   Q98PMO;
DT   01-OCT-2001 (Tremblrel. 18, Created)
DT   01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT   01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE   S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE)
DE   (ADOMET SYNTHETASE) (EC 2.5.1.6).
GN   MYPV_7020.
OS   Mycoplasma pulmonis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Molluscites;
OC   Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2107;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=UAB CTIP;
RX   MEDLINE=21267165; Pubmed=11353084;
RA   Chambeaud I., Heilig R., Ferris S., Barbe V., Samson D., Gallissot F.,
RA   Moszer I., Dybdvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA   Blanchard A.;
RT   "The complete genome sequence of the murine respiratory pathogen
    Mycoplasma pulmonis.";

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DN 01-DBC-2001 (TrEMBLrel. 19, last annotation update)
DE METK PROTEIN
GN METK OR L1N1773.
OS Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxId=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Franjeul L., Buchrieser C., Rusniok C., Amend A.,
  Baquero F., Berche P., Bloeker E., Brandt P., Chakraborty T.,
  Charbit A., Chetouni F., Couve E., de Berruier A., Deloux P.,
  Dornan E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
  Ertlin K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
  Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
  Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kurapat G.,
  Madano E., Maitournam A., Mata Vicente J., Ng E., Nedjati H.,
  Nordiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
  Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
  Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
  RT "Comparative genomics of Listeria species.";
  RL Science 294:849-852(2001).
  DR EMBL: AL596169; CAC97004.1; -.
  DR L1N1773; -.
  KW Complete proteome.
  SO SEQUENCE 399 AA; 43555 MW; 543905EDC51F3D90 CRC64;

alignment_scores:
  Quality: 61.00 Length: 18
  Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment_block:
US-09-198-779B-1 x Q92A25 ..

Align seg 1/1 to: Q92A25 from: 1 to: 399

169 AAGAGCGCGCATACGGCGCATTTGGCGCGTACGACGCGCATTCACCTG 218
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
368 GlnthralaalaahneglyhshpbclyArseraspseuduspLeuProTr 384

219 CGAG 222
|||
384 gplu 385

seq_name: sp_bacteriap:Q9KUP3

seq_documentation_block:
ID Q9KUP3 PRELIMINARY; PRT; 385 AA.
AC Q9KUP3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE S-ADENOSYLTRANSEFERONINE SYNTHETASE (EC 2.5.1.6) (METHYLONINE
DE ADENOSYLTRANSEFERASE) (ADOMET SYNTHETASE).
DE METK OR VC0472.
GN Vibri cholerae.
OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibri.
OC NCBI_TaxId=666;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
  Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
  Gali S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
  Ertolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
  McDonald L., Ueberlack T., Fleischmann R.D., Nierman W.C., White O.,
  Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
  Fraser C.M.;

```

alignment\_scores:

A	Hostln
A	Tajali

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,



RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003718; AAF55457.1; -.  
 DR FLYBase; FBgn0003013; osa.  
 DR InterPro; IPR001606; ARID.  
 DR InterPro; IPR002965; P\_rich\_extensn.  
 DR Pfam; PF01388; ARID; 1.  
 DR PRINTS; PR01217; PRICEXTNSN.  
 DR SMART; SM00501; BRIGHT; 1.  
 SQ SEQUENCE 2703 AA; 282894 MW; 27ED5BA0277A6369 CRC64;

alignment\_scores:                    Quality:       60.00                   Length:       22  
                                       Ratio:         3.529                   Gaps:         0  
 Percent Similarity: 77.273       Percent Identity: 54.545

alignment\_block:

US-09-198-779B-1/rev x Q9VEG7

Align seg 1/1 to: Q9VEG7 from: 1 to: 2703

```

84 AATAACACACGACGATGATGACGACCGTCATTATCAGCATGGGCA 35
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
46 ASnAsnAsnSerAsnAsnGlySerAspProSerIleGlnGlnGlnGlnI 62
   34 GCGTCGATCTGTCCAC 19
   |:::  ::  |||
   62 nAsnValAlaProHis 67
  
```

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OM of: US-09-198-779b-1 to: SwissProt\_40:\* out\_format : pfs  
Date: Aug 20, 2002 2:59 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

## Command line parameters:

-MODEL-frameat\_n2p\_model -DEV-xlp  
-O/cgn2\_1/USPRO.spool/US09198779/runat\_19082002.140913.25182/app-query.fasta.1.296  
-DB=SwissProt\_40 -QEMT=fastan -SUFFIX=rs -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELPO=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62  
-TRAS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pt  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pfs  
-NORWext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09198779.ecgn1\_1.23 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPXY -WAIT -THREADS=1

## Search information block:

Query: US-09-198-779b-1  
Query length: 235  
Database: SwissProt\_40:\*  
Database sequences: 105224  
Database length: 3819550  
Search time (sec): 21.730000

## score\_list:

Sequence	Strid	Orig	ZScore	Escore	Len	Documentation
SwissProt_40:METK_HORVU	+	127.00	318.60	1.2e-10	394	P50299 hordeum vulgare (barl)
SwissProt_40:METK_ACTCH	+	125.00	313.96	2.4e-10	360	P50303 actinidia chinensis (d)
SwissProt_40:METK_MESCR	+	122.00	305.15	6.8e-10	392	P93254 mesembryanthemum crys
SwissProt_40:METK_ARATH	+	120.00	299.73	1.4e-09	393	P23686 arabidopsis thaliana
SwissProt_40:METK_BRAJU	+	120.00	299.73	1.4e-09	393	P46511 brassica juncea (leaf
SwissProt_40:METK_CATRO	+	120.00	299.73	1.4e-09	393	P06551 catharanthus roseus (
SwissProt_40:METK_LYCES	+	120.00	299.73	1.4e-09	393	P42280 lycopersicon esculent
SwissProt_40:METK_LYCES	+	120.00	299.73	1.4e-09	393	P4281 lycopersicon esculent
SwissProt_40:METK_POPDE	+	120.00	299.69	1.4e-09	395	P47916 populus deltoides (pc
SwissProt_40:METL_ORYSA	+	118.00	294.31	2.7e-09	394	P93438 oryza sativa (rice).
SwissProt_40:METK_MUSAC	+	117.00	291.64	3.8e-09	393	O22338 musa acuminata (banan
SwissProt_40:METK_ORYSA	+	117.00	291.57	3.8e-09	396	P46511 oryza sativa (rice).
SwissProt_40:METK_PETCR	+	116.00	297.29	5.0e-09	145	P31156 petroselinum crispum
SwissProt_40:METK_PETCR	+	116.00	293.28	5.2e-09	234	P31155 petroselinum crispum
SwissProt_40:METK_PEA	+	116.00	289.54	5.4e-09	366	P49612 pisum sativum (garden F
SwissProt_40:METL_CATRO	+	116.00	288.94	5.4e-09	393	P06552 catharanthus roseus (
SwissProt_40:METL_ARATH	+	115.00	286.24	7.7e-09	393	P17562 arabidopsis thaliana
SwissProt_40:METK_PIBIN	+	103.00	253.86	4.9e-07	393	P50300 pinus banksiana (jack
SwissProt_40:METK_ACTCH	+	101.00	248.53	9.7e-07	390	P50301 actinidia chinensis (d
SwissProt_40:METK_PETRY	+	101.00	248.53	9.7e-07	390	P4498 petunia hybrida (petu
SwissProt_40:METL_LYCES	+	100.00	245.53	9.7e-07	390	P43282 lycopersicon esculent
SwissProt_40:METL_ACTCH	+	100.00	245.53	9.7e-07	390	P50302 actinidia chinensis (d
SwissProt_40:METL_DIACA	+	98.00	240.31	2.8e-06	396	P24260 dianthus caryophyllus
SwissProt_40:METK_CATRO	+	87.00	210.75	0.0001	390	P06553 catharanthus roseus (
SwissProt_40:METK_RICTY	+	75.00	178.55	0.0079	382	O91199 rickettsia typhi. s.d
SwissProt_40:METK_RICPR	+	74.00	175.90	0.0111	380	P56878 rickettsia prowazeki
SwissProt_40:METK_THEMA	+	74.00	175.57	0.0111	395	O9x198 thermotoga maritima.
SwissProt_40:METK_ACACA	+	68.00	159.53	0.0888	388	O95032 acanthamoeba castella
SwissProt_40:METK_BACSV	+	65.00	151.18	0.2513	400	P54419 bacillus subtilis. s
SwissProt_40:METK_SRSRT	+	64.00	148.26	0.3559	411	O9y492 streptomyces spectabi
SwissProt_40:METK_HUMAN	+	63.00	145.89	0.5016	395	P31155 homo sapiens (human).
SwissProt_40:METK_RAT	+	63.00	145.89	0.5016	395	P18288 rattus norvegicus (rat)
SwissProt_40:METK_MYCLE	+	63.00	145.72	0.5023	403	O9cc94 mycobacterium leprae.
SwissProt_40:METK_HELPJ	+	61.00	140.71	1.00	385	O9amns helicobacter pylori
SwissProt_40:METK_HELPJ	+	61.00	140.71	1.00	385	P56460 helicobacter pylori
SwissProt_40:METK_STRAU	+	61.00	140.45	1.00	393	P50307 staphylococcus aureus
SwissProt_40:METK_BACHD	+	61.00	140.41	1.00	399	O9r7q9 bacillus halodurans.
SwissProt_40:METK_LACIA	+	61.00	140.41	1.00	399	O9e6q9 lactococcus lactis (s
SwissProt_40:METK_MYCTV	+	61.00	140.33	1.00	403	P77899 mycobacterium tuberco
SwissProt_40:METK_SYNY3	+	60.50	138.51	1.20	426	P72871 synechocystis sp. (st

SwissProt\_40:METK\_TREPA + 59.00 135.08 2.00 396 | O83772 treponema pallidum  
SwissProt\_40:METL\_RAT + 59.00 135.06 2.00 397 | P13444 rattus norvegicus (r  
SwissProt\_40:METK\_BUCAT + 58.00 132.77 2.82 378 | P57486 buchnera aphidico  
SwissProt\_40:POLN\_SODV3 - 57.50 118.40 3.76 1788 | Q04544 southampton virus  
SwissProt\_40:CLT2\_HUMAN - 57.00 130.81 3.96 346 | Q9ns75 homo sapiens (hume

seq\_name: SwissProt\_40:METK\_HORVU

## seq\_documentation\_block:

ID	METK_HORVU	STANDARD:	PRT:	394 AA.
AC	P50299;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine			
DE	adenosyltransferase 1) (Adomet synthetase 1).			
GN	SMAL.			
OC	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;			
OC	Triticaceae; Hordeum.			
OX	NCBI_Taxid=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Mori S., Takizawa R.;			
RL	Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 285-322 FROM N.A.			
RC	TISSUE=ROOT.			
RA	Mori S., Takizawa R., Nakanishi H.;			
RL	Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM			
CC	METHIONINE AND ATP.			
CC	-1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +			
CC	diphosphate + S-adenosyl-L-methionine.			
CC	-1- PATHWAY: ACTIVATED METHYL CYCLE.			
CC	-1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; D63835; BAA09895.1; -.			
DR	EMBL; D49655; BAA08531.1; -.			
DR	HSSP; P04384; IMXB.			
DR	InterPro: IPR002133; S-Adomet-synt.			
DR	Pfam: PF00438; S-Adomet-synt. 1.			
DR	Pfam: PF02772; S-Adomet-syntD2; 1.			
DR	Pfam: PF02773; S-Adomet-syntD3; 1.			
DR	PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.			
DR	PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.			
KW	Transferase; One-carbon metabolism; Multigene family; ATP-binding.			
FT	NP_BIND 121 126 ATP (POTENTIAL).			
FT	BINDING 149 149 ATP (POTENTIAL).			
SQ	SEQUENCE 394 AA: 42841 MW: 2ED786F33530013 CRC64;			

## alignment\_scores:

Quality:	127.00	Length:	25
Ratio:	5.292	Gaps:	0
Percent Similarity:	96.000	Percent Identity:	96.000

## alignment\_block:

US-09-198-779b-1 x METK\_HORVU ..

Align seg 1/1 to: METK\_HORVU from: 1 to: 394

160 AGGTTTCATCAAGACCGCCGATACGGCCACTTGGCCGTGACGACCGCA 209  
|||||

362 ArgpHeilelysthrAlaalaTyrglyHsPheGlyArgAspAspAlaAs 378  
210 CTTCACTGAGGAGGTCGTCACGCC 234  
||||| |||||||  
378 pPheHTrpGluValValysPro 386

seq\_name: SwissProt\_40:METM\_ACTCH

seq\_documentation\_block:

ID METM\_ACTCH STANDARD; PRT; 360 AA.  
AC P50303;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE S-adenosylmethionine synthetase 3 (EC 2.5.1.6) (Methionine  
adenosyltransferase 3) (Adomet synthetase 3) (Fragment).  
OS Actinidia chinensis (Kiwi) (Actinidia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; Ericales; Actinidiaceae; Actinidia.  
OX NCBI\_Taxid=3625;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=95357424; PubMed=7630953;  
RA Wiltaker D.J., Smith G.S., Gardner R.C.;  
RT "Three cDNAs encoding S-adenosyl-L-methionine synthetase from  
RT Actinidia chinensis".  
RL Plant Physiol. 108:1307-1308(1995).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
CC METHIONINE AND ATP.  
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
CC diphosphate + S-adenosyl-L-methionine.  
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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CC  
DR EMBL: U17241; AAA81379.1; -  
DR HSSP: P04384; IMXB.  
DR InterPro: IPR002133; S-Adomet\_synt.  
DR Pfam: PF00438; S-Adomet\_synt.1.  
DR Pfam: PF02772; S-Adomet\_syntD2; 1.  
DR Pfam: PF02773; S-Adomet\_syntD3; 1.  
DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.  
FT NON\_TER 1 1  
FT NP\_BIND 86 91 ATP (POTENTIAL).  
FT BINDING 114 114 ATP (POTENTIAL).  
SQ SEQUENCE 360 AA; 39513 MW; E8B2626FE6E71171 CRC64;

alignment\_scores:

Quality: 125.00 Length: 25  
Ratio: 5.208 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 92.000

alignment\_block:

US-09-198-779b-1 x METM\_ACTCH ..

Align seg 1/1 to: METM\_ACTCH from: 1 to: 360

160 AGGTTTCATCAAGACCGCCGATACGGCCACTTTGGCCGTAGCAGCGCGA 209  
|||||:|||||  
328 ArgPheIeuLysThrAlaAlaTyrglyHsPheGlyArgAspAspAlaAs 344  
210 CTTCACTGAGGAGGTCGTCACGCC 234

||||| |||||||  
344 pPheHTrpGluValValysPro 352

seq\_name: SwissProt\_40:METK\_MESCR

seq\_documentation\_block:

ID METK\_MESCR STANDARD; PRT; 392 AA.  
AC P93254;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
adenosyltransferase) (Adomet synthetase).  
OS Mesembryanthemum crystallinum (Common ice plant).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.  
OX NCBI\_Taxid=3544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Michalowski C.B., Bohnert H.J.;  
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
CC METHIONINE AND ATP (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
CC diphosphate + S-adenosyl-L-methionine.  
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
DR EMBL: U79767; AAB38500.1; -  
DR HSSP: P04384; IMXB.  
DR InterPro: IPR002133; S-Adomet\_synt.  
DR Pfam: PF00438; S-Adomet\_synt.1.  
DR Pfam: PF02772; S-Adomet\_syntD2; 1.  
DR Pfam: PF02773; S-Adomet\_syntD3; 1.  
DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.  
FT NP\_BIND 119 124 ATP (POTENTIAL).  
FT BINDING 147 147 ATP (POTENTIAL).  
SQ SEQUENCE 392 AA; 42885 MW; D13C2CD03757165A CRC64;

alignment\_scores:

Quality: 122.00 Length: 25  
Ratio: 5.083 Gaps: 0  
Percent Similarity: 96.000 Percent Identity: 88.000

alignment\_block:

US-09-198-779b-1 x METK\_MESCR ..

Align seg 1/1 to: METK\_MESCR from: 1 to: 392

160 AGGTTTCATCAAGACCGCCGATACGGCCACTTTGGCCGTAGCAGCGCGA 209  
|||||:|||||  
360 ArgTyrlEuLysThrAlaAlaTyrglyHsPheGlyArgAspAspAlaAs 376

210 CTTCACTGAGGAGGTCGTCACGCC 234

376 pPheHTrpGluValValysPro 384

seq\_name: SwissProt\_40:METK\_ARATH

seq\_documentation\_block:

ID METK\_ARATH STANDARD; PRT; 393 AA.

160 AGGTTTCATCAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209  
 |||||:::|||||  
 361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377

160 AGGTTATCATCAAGACCGCCGCATACGGCACCTTGGCCGTGACGACGCCGA 209  
|||||:::|||||  
361 ArgPheLeuIysThrAlaAlaIleYrGIySPheGlyArgAspProAs 377  
210 CTTTCACCTGCGAGGTGTAAACCC 234



```

seq_documentation_block:
ID METL_LYCES STANDARD: PRT: 393 AA.
AC P43281;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
adenosyltransferase 2) (Adomet synthetase 2).
GN SAM2.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasteridae I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. RUTGERS;
RX MEDLINE=94289646; PubMed=8018871;
RA Espartero J., Pintor-Toro J.A., Pardo J.M.;
RT "Differential accumulation of S-adenosylmethionine synthetase
transcripts in response to salt stress.";
RL Plant Mol. Biol. 25:217-227(1994).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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CC -----
DR EMBL: Z24742; CAA80866.1; -
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt.1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE; One-carbon metabolism; Multigene family; ATP-binding.
KW NP_BIND 119 124
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 393 AA; 43081 MW; 4E77DD01B21BFD79 CRC64;

alignment_scores:
Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:
US-09-198-779b-1 x METL_LYCES ..
Align seg 1/1 to: METL_LYCES from: 1 to: 393

160 AGGTCATCAAGACCGCGCATAGCGGCGTGGCGGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 ArgpHeuLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 377
210 CTTACACCTGCAGAGGTGTCAGACCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 pPheThrTrpGluValValLysPro 385

seq_name: SwissProt_40:METK_POPDE
seq_documentation_block:

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ID METK_POPDE STANDARD: PRT: 395 AA.
AC P47916;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
adenosyltransferase) (Adomet synthetase).
GN Populus deltoides (Poplar).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=3696;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf.
RX MEDLINE=94105359; PubMed=8278561;
RA van Doorslaere J., Gieles J., van Montagu M., Inze D.;
RT "A cDNA encoding S-adenosyl-L-methionine synthetase from poplar.";
RL Plant Physiol. 102:1365-1366(1993).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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CC -----
DR EMBL: M73430; AAA20112.1; -
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt.1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE; One-carbon metabolism; Multigene family; ATP-binding.
KW NP_BIND 120 125
FT BINDING 148 148 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 43269 MW; 6E90404CE1CD0FC6 CRC64;

alignment_scores:
Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:
US-09-198-779b-1 x METK_POPDE ..
Align seg 1/1 to: METK_POPDE from: 1 to: 395

160 AGGTCATCAAGACCGCGCATAGCGGCGTGGCGGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
362 ArgpHeuLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 378
210 CTTACACCTGCAGAGGTGTCAGACCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 pPheThrTrpGluValValLysPro 386

seq_name: SwissProt_40:METL_ORYSA
seq_documentation_block:
ID METL_ORYSA STANDARD: PRT: 394 AA.
AC P93458;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, TAICHUNG.
RX MEDLINE=95062735; PubMed-7972513;
RA van Breusegem F., Dekeyser R., Giejen J., van Montagu M.,
RT Caplan A.;
RT "Characterization of a S-adenosylmethionine synthetase gene in rice.";
RL Plant Physiol. 105:1463-1464(1994).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z26867; CA81481.1; -.
DR HSSP; P04384; IMXB.
DR ANU-2DPAGE; P46611; -.
DR InterPro; IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth.1.
DR Pfam; PF02772; S-Adomet_synth2; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
FT BINDING 122 127 ATP (POTENTIAL).
FT BINDING 150 150 ATP (POTENTIAL).
SQ SEQUENCE 396 AA; 43220 MW; 16FE43474045FEB9 CRC64;

alignment_scores:
Quality: 117.00 Length: 25
Ratio: 5.087 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METK_ORYSA ..
Align seg 1/1 to: METK_ORYSA from: 1 to: 396

160 AGGTTTCATCAAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 ArgTyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 380
210 CTTCACTCGCAGGCGTGTCAAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
380 pPheThrTrpGluValValLysPro 388

seq_name: SwissProt_40:METL_PETCR

seq_documentation_block:
ID METL_PETCR STANDARD; PRT; 145 AA.
AC P31156;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (Adomet synthetase 2) (Fragment).
GN SMS-2.
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX NCBI_TaxID=4043;
RN [1]
RP SEQUENCE FROM N.A.
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RP SEQUENCE FROM N.A.
RC TISSUE=leaf;
RX MEDLINE=92262510; PubMed=1374911;
RA Kwaileck P., Plesch G., Hahlbrock K., Somssich I.E.;
RT "Induction by fungal elicitor of S-adenosyl-L-methionine synthetase
RT and S-adenosyl-L-homocysteine hydrolyase mRNAs in cultured cells and
RT leaves of Petroselinum crispum.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4713-4717(1992).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- TISSUE SPECIFICITY: MAINLY IN FLORAL BUDS AND ROOTS.
CC -1- INDUCTION: BY FUNGAL ELICITOR.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62757; AAA33858.1; -.
DR HSSP; P04384; IMXB.
DR InterPro; IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth.1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; PARTIAL.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
FT TRANS 1 1
FT TRANS 145 AA; 15758 MW; 900FEB6A472EB08 CRC64;
SQ SEQUENCE 145 AA; 15758 MW; 900FEB6A472EB08 CRC64;

alignment_scores:
Quality: 116.00 Length: 25
Ratio: 5.043 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METL_PETCR ..
Align seg 1/1 to: METL_PETCR from: 1 to: 145

160 AGGTTTCATCAAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
115 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAs 131
210 CTTCACTCGCAGGCGTGTCAAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 pPheThrTrpGluValValLysPro 139

seq_name: SwissProt_40:METK_PETCR

seq_documentation_block:
ID METK_PETCR STANDARD; PRT; 234 AA.
AC P31155;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 1) (Adomet synthetase 1) (Fragment).
GN SMS-1.
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX NCBI_TaxID=4043;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE=Leaf; PubMed=1374911;
RX MEDLINE=92262510;
RA Kawalleck P., Plesch G., Hahlbrock K., Somssich I.E.:
RT "Induction by fungal elicitor of S-adenosyl-L-methionine synthetase
RT and S-adenosyl-L-homocysteine hydrolase mRNAs in cultured cells and
RT leaves of Petroselinum crispum."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4713-4717(1992).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- TISSUE SPECIFICITY: MAINLY IN FLORAL BUDS AND ROOTS.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M62758; AAA33857.1; -.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth2; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; PARTIAL.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NON_TER 1
FT BINDING 1
FT BINDING 234 AA; 25652 MW; 8491086FA5D16BDA CRC64;
SQ SEQUENCE 234 AA; 25652 MW; 8491086FA5D16BDA CRC64;

alignment_scores:
Quality: 116.00 Length: 25
Ratio: 5.043 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METK_PETCR ..
Align seg 1/1 to: METK_PETCR from: 1 to: 234

160 AGGTTTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 ArgPheLeuYstHrAlaIatYrGlyHisPheGlyArgGluAspProAs 220
210 CTTACCTGCGAGGTGTCAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
220 PHeHTrpGluValValysPro 228

seq_name: SwissProt_40:METK_PEA

seq_documentation_block:
ID METK_PEA STANDARD; PRT; 366 AA.
AC P49612;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 1) (Adomet synthetase 1) (Fragment).
GN SAM51.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
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```
RC STRAIN=CV ALASKA;
RX MEDLINE=96194463; PubMed=8624412;
RA Gomez L., Carrasco P.:
RT "Hormonal regulation of S-adenosylmethionine synthase transcripts in
RT pea ovaries."
RL Plant Mol. Biol. 30:821-832(1996).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X82076; CAA57580.1; -.
DR HSSP: L36680; AAA58772.1; ALT_SEQ.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NON_TER 1
FT BINDING 94
FT BINDING 99
FT BINDING 122
FT BINDING 122 ATP (POTENTIAL).
SQ SEQUENCE 366 AA; 39939 MW; EDB446F5D407627 CRC64;

alignment_scores:
Quality: 116.00 Length: 25
Ratio: 5.043 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METK_PEA ..
Align seg 1/1 to: METK_PEA from: 1 to: 366

160 AGGTTTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
336 ArgPheLeuYstHrAlaIatYrGlyHisPheGlyArgGluAspProAs 352
210 CTTACCTGCGAGGTGTCAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
352 PHeHTrpGluValValysPro 360

seq_name: SwissProt_40:METL_CATRO

seq_documentation_block:
ID METL_CATRO STANDARD; PRT; 393 AA.
AC Q96552;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (Adomet synthetase 2).
GN SAM52.
OS Cathartanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
OC Vincaceae; Cathartanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RP SEQUENCE FROM N.A.
RX MEDLINE-9718855; PubMed-9037140;
RA Schroeder G., Eichel J., Breinig S., Schroeder J.;
RT "Three differentially expressed S-adenosylmethionine synthetases from
RL Catharanthus roseus: molecular and functional characterization.",
  Plant Mol. Biol. 33:211-222(1997).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
  METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z71272; CAA95857.1; -.
DR HSSP: P04384; LMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt.1.
DR Pfam: PF02772; S-Adomet_syntD2; 1.
DR Pfam: PF02773; S-Adomet_syntD3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KM Transferrase: One-carbon metabolism: Methylgene family: ATP-binding.
FT NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 393 AA; 43004 MW; 4A9070B5B9B783D CRC64;

alignment_scores:
  Quality: 116.00 Length: 25
  Ratio: 5.043 Gaps: 0
  Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779b-1 x METL_CATRO ..

Align seg 1/1 to: METL_CATRO from: 1 to: 393

160 AGGTTTCATCAAGACCGGCATACGCGCATTGCGCGTGACGACGCGCA 209
  |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
361 ATGPhenulysthriAlaAlaATyGlyHISPhenylArgGluAspProAs 377
210 CTTTCACCTCGCGAGGTGTCACGCCC 234
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
377 pPhetHrTpIolValValIallysPro 385

seq_name: SwissProt_40:METL_ARATH

seq_documentation_block:
ID METL_ARATH STANDARD; PRT; 393 AA.
AC P17562; Q42263;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
  adenosyltransferase 2) (Adomet synthetase 2).
GN SAM2 OR ATAG01850 OR T7811.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE-90128280; PubMed-2482229;

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RA Pelerman J., Saito K., Cottyn B., Engler G., Seurinck J.,
  van Montagu M., Inze D.;
RT "Structure and expression analyses of the S-adenosylmethionine
  synthetase gene family in Arabidopsis thaliana.",
  Gene 84:359-369(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE-20083488; PubMed-10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
  Pohl T., Duesterhoeft A., Stiekema W., Ertlan K.-D., Terry N.,
  Harris B., Ansoorge W., Brandt P., Grievell L.B., Rieger M.,
  Weichselgartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
  Kreis M., Delsenay M., Puigdomenech P., Watson M., Schmidthein T.,
  Reichert B., Portetelle D., Perez-Alonso M., Bottry M., Bancroft I.,
  Vos P., Hohnel S., Zimmermann W., Wedler H., Ridley P.,
  Langham S.-A., McCullagh B., Blham L., Robben J.,
  van der Schuren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
  Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
  Weitzengger T., Botne G., Ramsperger U., Hilbert H., Braun M.,
  Holzner E., Brandt A., Peters S., van Staveren M., Dirke W.,
  Moellman P., Klein lankhorst R., Rose M., Hauf J., Koetter P.,
  Berner S., Hempel S., Feldpausch M., Lambert S., Van den Daele H.,
  De Keyser A., Buyschaert C., Gielen J., Villarreal R., De Clercq R.,
  Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
  Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
  Pettit A., Rajandream M.A., Lyne M., Bennis V., Rechmann S.,
  Borokva D., Blocker H., Scharfe M., Grimm M., Loehner T.-H.,
  Dose S., de Haan M., Maarse A.C., Schefer M., Mueller-Auer S.,
  Gabel C., Fuchs M., Partmann B., Granderath K., Danner D., Herzi A.,
  Neumann S., Argitlou A., Vitale D., Liguori R., Pivardi E.,
  Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
  Schabli S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
  Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
  Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
  Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
  Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielek C.,
  Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
  Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
  Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
  Sekhon M., Murray J., Sheet P., Cordes M., Abu-Friedeh J.,
  Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
  Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
  Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
  Kramer J., Fulton L., Mardis E., Dante M., Peglin K., Hillier L.,
  Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
  du H., Ali J., Berghoff A., Jones K., Drome K., Cotton M., Joshi C.,
  Antoniou B., Zidanac M., Strong C., Sun H., Lamar B., Yordan C.,
  Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
  Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
  Grant S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
  Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
  thaliana.",
  Nature 402:769-777(1999).
RN [3]
RP SEQUENCE OF 141-248 AND 322-393 FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE=Seedling;
RA Desprez T., Amselem J., Chiappello H., Caboche M., Hofte H.;
  Submitted (MAY-1994) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
  METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- MISCELLANEOUS: IN A. THALIANA, THERE ARE TWO GENES ENCODING THIS
  PROTEIN (SAM1 AND SAM2).
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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DR EMBL; M33217; AAA32869.1; -
DR EMBL; AC007138; AAD22647.1; -
DR EMBL; AL161493; CAB80678.1; -
DR EMBL; Z33778; CAAB3930.1; -
DR EMBL; Z29136; CAAB2393.1; -
DR PIR; J00410; J00410.
DR HSSP; P04384; IMXB.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF00438; S-AdoMet_synth. 1.
DR Pfam; PF02772; S-AdoMet_synth2; 1.
DR Pfam; PF02773; S-AdoMet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
KW NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 393 AA; 43255 MW; CE008EA565FD1FBC CRC64;
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alignment\_scores:

Quality:	115.00	Length:	25
Ratio:	5.227	Gaps:	0
Percent Similarity:	88.000	Percent Identity:	88.000

alignment\_block:

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US-09-198-779B-1 x METL_ARATH ..
Align seg 1/1 to: METL_ARATH from: 1 to: 393
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160 AGGTCATCAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGA 209
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361 ArgPheGlnLysThrAlaAlaIleTyrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACTCGCAGGTGTCAAGCCC 234
||||| ||||||| |||||||
377 PheThrTrpGluValValLysPro 385
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seq\_name: SwissProt\_40:METK\_P1NBN

seq\_documentation\_block:

ID	METK_P1NBN	STANDARD;	PRT;	393 AA.
AC	P50300;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine			
DE	adenosyltransferase) (Adomet synthetase).			
OS	Pinus banksiana (Jack pine).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.			
OX	NCBI_TaxID=3353;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Root;			
RA	Mayne M.B., Coleman J.R., Blumwald E.;			
RL	Submitted (OCT-1995) to the EMBL/Genbank/DBJ databases.			
CC	- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM			
CC	METHIONINE AND ATP.			
CC	- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +			
CC	diphosphate + S-adenosyl-L-methionine.			
CC	- PATHWAY: ACTIVATED METHYL CYCLE.			
CC	- TISSUE SPECIFICITY: ROOT.			
CC	- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .			
CC	-----			

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CC or send an email to license@isb-sib.ch).
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DR EMBL; U38186; AA79831.1; -
DR HSSP; P04384; IMXB.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF00438; S-AdoMet_synth. 1.
DR Pfam; PF02772; S-AdoMet_synth2; 1.
DR Pfam; PF02773; S-AdoMet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
KW NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 393 AA; 43168 MW; D12F7BP9B634185E CRC64;
```

alignment\_scores:

Quality:	103.00	Length:	22
Ratio:	5.150	Gaps:	0
Percent Similarity:	90.909	Percent Identity:	86.364

alignment\_block:

```
US-09-198-779B-1 x METK_P1NBN ..
Align seg 1/1 to: METK_P1NBN from: 1 to: 393
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```
169 AAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACTG 218
||||| ||||||| ||||||| ||||||| ||||||| |||||||
364 LysThrAlaIleTyrGlyHisPheGlyArgAspAspProAspPheThr 380
219 CGAGGTGTCAAGCCC 234
||||| ||||||| |||||||
380 PglutThrValLysPro 385
```

seq\_name: SwissProt\_40:METK\_ACTCH

seq\_documentation\_block:

ID	METK_ACTCH	STANDARD;	PRT;	390 AA.
AC	P50301;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine			
DE	adenosyltransferase 1) (Adomet synthetase 1).			
OS	Actinidia chinensis (Kiwi) (Yangtiao).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; Ericales; Actinidiaceae; Actinidia.			
OX	NCBI_TaxID=3625;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95357424; PubMed=7630953;			
RA	Whittaker D.J., Smith G.S., Gardner R.C.;			
RL	"Three cDNAs encoding S-adenosyl-L-methionine synthetase from			
RL	Actinidia chinensis".			
RL	Plant Physiol. 108:1307-1308(1995).			
CC	- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM			
CC	METHIONINE AND ATP.			
CC	- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +			
CC	diphosphate + S-adenosyl-L-methionine.			
CC	- PATHWAY: ACTIVATED METHYL CYCLE.			
CC	- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			

```
DR HSSP: P04384; 1MXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE: One-carbon metabolism; Multigene family; ATP-binding.
FT BINDING 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 390 AA; 42519 MW; E3B6B10112B1E31 CRC64;

alignment_scores:
  Quality: 101.00      Length: 24
  Ratio: 4.810        Gaps: 0
Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:
US-09-198-779B-1 x METK_ACTCH ..

Align seg 1/1 to: METK_ACTCH from: 1 to: 390

160 AGGTTGATCAGACCGCGCATACGCCACTTGCGCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgTyrGlnLysThrAlaIatrglyHisPheGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCTCAAG 231
||||| ||||||| ||||||| ||||||| ||
377 pPheThrTrpGlnThrValLys 384

seq_name: SwissProt_40:METK_PETHY

seq_documentation_block:
ID METK_PETHY STANDARD: PRT; 390 AA.
AC P48498;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
  adenosyltransferase) (Adomet synthetase).
GN SAM1.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
  Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. V-26; TISSUE=Corolla;
RX MEDLINE=95334508; PubMed=7610179;
RA Izhaki A., Shoseyov O., Weiss D.;
RT Plant Physiol. 108:841-842(1995).
RL
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
  METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL: X82214; CAA57696.1; -.
DR HSSP: P04384; 1MXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
```

```
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE: One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 390 AA; 42765 MW; F49DBE8E9F6605B CRC64;

alignment_scores:
  Quality: 101.00      Length: 24
  Ratio: 4.810        Gaps: 0
Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:
US-09-198-779B-1 x METK_PETHY ..

Align seg 1/1 to: METK_PETHY from: 1 to: 390

160 AGGTTGATCAGACCGCGCATACGCCACTTGCGCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgTyrGlnLysThrAlaIatrglyHisPheGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCTCAAG 231
||||| ||||||| ||||||| ||||||| ||
377 pPheThrTrpGlnThrValLys 384

seq_name: SwissProt_40:METK_LYCES

seq_documentation_block:
ID METK_LYCES STANDARD: PRT; 390 AA.
AC P43282;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE S-adenosylmethionine synthetase 3 (EC 2.5.1.6) (Methionine
  adenosyltransferase 3) (Adomet synthetase 3).
GN SAM3.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Rutgers;
RX MEDLINE=94289646; PubMed=8018871;
RA Espartero J., Pintor-Toro J.A., Pardo J.M.;
RT "Differential accumulation of S-adenosylmethionine synthetase
  transcripts in response to salt stress.";
RL Plant Mol. Biol. 25:217-227(1994).
RL
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
  METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL: Z24743; CAA80867.1; -.
DR HSSP: P04384; 1MXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
```

DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW Transferrase: One-carbon metabolism; Multigene family; ATP-binding.  
 FT NP\_BIND 119 124 ATP (POTENTIAL).  
 FT BINDING 147 147 ATP (POTENTIAL).  
 SQ SEQUENCE 390 AA; 42652 MW; C1FBC513C81CA992 CRC64;

alignment\_scores:  
 Quality: 101.00 Length: 24  
 Ratio: 4.810 Gaps: 0  
 Percent Similarity: 87.500 Percent Identity: 79.167

## alignment\_block:

US-09-198-779B-1 x METM\_LYCES

Align seg 1/1 to: METM\_LYCES from: 1 to: 390

160 AGGTCATCAAGACCGCCGATACGCCACTTGGCCGTGACGACGCCGA 209  
 ||||| |||||  
 361 ArgTYGInLysThrAlaAlaIatYrGLyHisPheGLyArgAspAspAlaAs 377  
 210 CTTACCGTCGAGGTGTCAG 231  
 ||||| |||||  
 377 PLeuThrTrpGIuThrValLys 384

seq\_name: SwissProt\_40:METL\_ACTCH

## seq\_documentation\_block:

ID METL\_ACTCH STANDARD; PRT; 390 AA.  
 AC P50302;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine  
 adenosyltransferase 2) (Adomet synthetase 2).  
 OS Actinidia chinensis (Kiwai) (Yangtze).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Ericales; Actinidiaceae; Actinidia.  
 OX NCBI\_TaxID=3625;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95357424; PubMed=7630953;  
 RA Whittaker D.J., Smith G.S., Gardner R.C.;  
 RT "Three cDNAs encoding S-adenosyl-L-methionine synthetase from  
 Actinidia chinensis.";  
 RL Plant Physiol. 108:1307-1308(1995).  
 CC -!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 METHIONINE AND ATP.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 S-adenosyl-L-methionine.  
 CC -!- PATHWAY: ACTIVATED METHYL CYCLE.  
 CC -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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 CC -----  
 CC EMBL: U17239; AAA81377.1; -  
 DR HSSP: P04384; IMXB.  
 DR InterPro: IPR002133; S-Adomet\_synt.  
 DR Pfam: PF00438; S-Adomet\_synt. 1.  
 DR Pfam: PF02772; S-Adomet\_synt2; 1.  
 DR Pfam: PF02773; S-Adomet\_synt3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW Transferrase: One-carbon metabolism; Multigene family; ATP-binding.  
 FT NP\_BIND 119 124 ATP (POTENTIAL).  
 SQ SEQUENCE 390 AA; 43189 MW; 959024A69865E2D9 CRC64;

FT BINDING 147 147 ATP (POTENTIAL).  
 SQ SEQUENCE 390 AA; 42607 MW; ABB76AE7FB87270F CRC64;

alignment\_scores:  
 Quality: 100.00 Length: 24  
 Ratio: 4.545 Gaps: 0  
 Percent Similarity: 91.667 Percent Identity: 79.167

## alignment\_block:

US-09-198-779B-1 x METL\_ACTCH

Align seg 1/1 to: METL\_ACTCH from: 1 to: 390

160 AGGTCATCAAGACCGCCGATACGCCACTTGGCCGTGACGACGCCGA 209  
 ||||| |||||  
 361 ArgTYGInLysThrAlaAlaIatYrGLyHisPheGLyArgAspAspAlaAs 377  
 210 CTTACCGTCGAGGTGTCAG 231  
 ||||| |||||  
 377 PLeuThrTrpGIuThrValLys 384

seq\_name: SwissProt\_40:METL\_DIACA

## seq\_documentation\_block:

ID METL\_DIACA STANDARD; PRT; 396 AA.  
 AC P24260;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine  
 adenosyltransferase 2) (Adomet synthetase 2).  
 OS Dianthus caryophyllus (Carnation) (Clove pink).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Dianthus.  
 OX NCBI\_TaxID=3570;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Larsen P.B., Woodson W.R.;  
 RT "Cloning and nucleotide sequence of a S-adenosylmethionine synthetase  
 RT cDNA clone from carnation.";  
 RL Plant Physiol. 96:997-998(1991).  
 CC -!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 METHIONINE AND ATP.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 S-adenosyl-L-methionine.  
 CC -!- PATHWAY: ACTIVATED METHYL CYCLE.  
 CC -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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 CC -----  
 CC EMBL: M61882; AAA33274.1; -  
 DR HSSP: P04384; IMXB.  
 DR InterPro: IPR002133; S-Adomet\_synt.  
 DR Pfam: PF00438; S-Adomet\_synt. 1.  
 DR Pfam: PF02772; S-Adomet\_synt2; 1.  
 DR Pfam: PF02773; S-Adomet\_synt3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW Transferrase: One-carbon metabolism; Multigene family; ATP-binding.  
 FT NP\_BIND 123 128 ATP (POTENTIAL).  
 FT BINDING 151 151 ATP (POTENTIAL).  
 SQ SEQUENCE 396 AA; 43189 MW; 959024A69865E2D9 CRC64;

alignment\_scores:  
Ratio: 98.00 Length: 24  
Gaps: 0  
Percent Similarity: 91.667 Percent Identity: 70.833

## alignment\_block:

US-09-198-779B-1 x METL\_DIACA ..

Align seg 1/1 to: METL\_DIACA from: 1 to: 396

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160 AGGTCATCAAGACCGCCGATACGCCACTTTGGCCGTGACGACGCCGA 209
|||||  |||||||  |||||||  |||||||  |||||||  ||
364 ArgTyrlEuLysThrAlaAlaLeuGlyHisPheGlyArgGluAspProAs 380
210 CTTCACCTGCGAGGTGTCACG 231
|||||  |||||||  |||||||  |||||||  |||||||  ||
380 PheThrTrpGluThrValValys 387
```

seq\_name: SwissProt\_40:METW\_CATRO

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seq_documentation_block:
ID METW_CATRO STANDARD; PRT; 390 AA.
AC 096553;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE S-adenosylmethionine synthetase 3 (EC 2.5.1.6) (Methionine
  adenosyltransferase 3) (Adomet synthetase 3).
GN SAM53.
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
  OC Vincaceae; Catharanthus.
OX NCBI_TaxId=4056;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97188555; PubMed=9037140;
RT Schroeder G., Eichel J., Breinld S., Schroeder J.;
  "Three differentially expressed S-adenosylmethionine synthetases from
  Catharanthus roseus: molecular and functional characterization.";
  RL Plant Mol. Biol. 33:211-222(1997).
CC -! FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
  METHIONINE AND ATP.
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -! PATHWAY: ACTIVATED METHYL CYCLE.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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  CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 271273; CAB5958.1; .
CC HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth.1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 390 AA; 42556 MW; 41E0BD8FA84DF776 CRC64;
```

alignment\_scores: Quality: 87.00

Length: 24

Ratio: 4.350 Gaps: 0  
Percent Similarity: 83.333 Percent Identity: 70.833

## alignment\_block:

US-09-198-779B-1 x METW\_CATRO ..

Align seg 1/1 to: METW\_CATRO from: 1 to: 390

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160 AGGTCATCAAGACCGCCGATACGCCACTTTGGCCGTGACGACGCCGA 209
|||||  |||||||  |||||||  |||||||  |||||||  ||
361 ArgTyrlGlyThrAlaAlaLeuGlyHisLeuGlyArgAspAspProAs 377
210 CTTCACCTGCGAGGTGTCACG 231
|||||  |||||||  |||||||  |||||||  |||||||  ||
377 PheThrTrpGluThrValValys 384
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seq\_name: SwissProt\_40:METK\_RICTY

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seq_documentation_block:
ID METK_RICTY STANDARD; PRT; 382 AA.
AC 09RL99;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
  adenosyltransferase) (Adomet synthetase) (MAT).
GN METK.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
  OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxId=785;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATLWNINGTON;
RX MEDLINE=99416441; PubMed=10486973;
RT Andersson J.O., Andersson S.G.E.;
  "Genome degradation is an ongoing process in Rickettsia.";
  RL Mol. Biol. Evol. 16:1178-1191(1999).
CC -! FUNCTION: Catalyzes the formation of S-adenosylmethionine from
  methionine and ATP. The overall synthetic reaction is composed of
  CC two sequential steps, Adomet formation and the subsequent
  CC triphosphate hydrolysis which occurs prior to release of
  CC Adomet from the enzyme (By similarity).
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -! COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
  bind per subunit (By similarity).
CC -! PATHWAY: Activated methyl cycle.
CC -! SUBUNIT: Homotrimer (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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  CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
  CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ238757; CAB56109.1; .
CC HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth.1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; ATP-binding; Magnesium.
FT NP_BIND 260 267 ATP (POTENTIAL).
FT METAL 17 17 MAGNESIUM (BY SIMILARITY).
FT METAL 272 272 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42257 MW; 3157612AC8BD681 CRC64;
```



alignment\_scores:  
 Quality: 75.00 Length: 18  
 Ratio: 4.688 Gaps: 0  
 Percent Similarity: 88.889 Percent Identity: 72.222

## alignment\_block:

US-09-198-779B-1 x METK\_RICTY

Align seg 1/1 to: METK\_RICTY from: 1 to: 382

169 AAGACCCGCGATACGCCACTTGGCCGTGACGACGCCGACCTTCACCTG 218  
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||  
 354 LysThrAlaSerTyrGlyHisPheGlyArgGluAspGluAsnPheThrTr 370

219 CGAG 222  
 |||  
 370 pGlu 371

seq\_name: SwissProt\_40:METK\_RICPR

## seq\_documentation\_block:

ID METK\_RICPR STANDARD; PRT; 380 AA.

AC P56878;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
 adenosyltransferase) (Adomet synthetase) (MAT).  
 GN METK OR RP777.  
 OS Rickettsia prowazekii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID-782;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-MADRID E;  
 RX MEDLINE-99039499; PubMed-9823893;  
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,  
 RA Sicheitiz-Ponten T., Alsmark U.C.M., Podowski R.M., Naslund A.K.,  
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
 RT "The genome sequence of Rickettsia prowazekii and the origin of  
 RT mitochondria.";  
 RT Nature 396:133-140(1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN-B;  
 RX MEDLINE-99416441; PubMed-10486973;  
 RA Andersson J.O., Andersson S.G.E.;  
 RT "Genome degradation is an ongoing process in Rickettsia.";  
 RT Mol. Biol. Evol. 16:1178-1191(1999).  
 CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 CC methionine and ATP. The overall synthetic reaction is composed of  
 CC two sequential steps, Adomet formation and the subsequent  
 CC triphosphatase hydrolysis which occurs prior to release of  
 CC Adomet from the enzyme (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC dihydrophosphate + S-adenosyl-L-methionine.  
 CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion  
 CC bind per subunit (By similarity).  
 CC -1- PATHWAY: Activated methyl cycle.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 CC -1- CAUTION: METK IS NON FUNCTIONAL IN STRAIN MADRID E WHOSE COMPLETE  
 CC GENOME HAS BEEN SEQUENCED. IT IS INTERRUPTED BY A STOP CODON IN  
 CC POSITION 141.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC DR EMBL: AJ235273; -; NOT ANNOTATED\_CDS.  
 CC DR EMBL: AJ238756; CAB56090.1; -.

DR HSSP: P04384; 1MXB.  
 DR InterPro: IPR002133; S-Adomet\_synt.

DR Pfam: PF00458; S-Adomet\_synt; 1.  
 DR Pfam: PF02772; S-Adomet\_synt2; 1.  
 DR Pfam: PF02773; S-Adomet\_synt3; 1.

DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.

KW Transferase, One-carbon metabolism; ATP-binding; Magnesium;  
 KW Complete proteome.

FT NP\_BIND 260 267 APP (POTENTIAL).  
 FT METAL 17 17 MAGNESIUM (BY SIMILARITY).  
 FT METAL 272 272 MAGNESIUM (BY SIMILARITY).

FT METAL 272 272 MAGNESIUM (BY SIMILARITY).  
 SQ SEQUENCE 380 AA: 42149 MW: DIB29BB64481FECA CRC64;

## alignment\_scores:

Quality: 74.00 Length: 18  
 Ratio: 4.625 Gaps: 0  
 Percent Similarity: 88.889 Percent Identity: 72.222

## alignment\_block:

US-09-198-779B-1 x METK\_RICPR

Align seg 1/1 to: METK\_RICPR from: 1 to: 380

169 AAGACCCGCGATACGCCACTTGGCCGTGACGACGCCGACCTTCACCTG 218  
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||  
 354 LysThrAlaSerTyrGlyHisPheGlyArgGluAspGluAsnPheThrTr 370

219 CGAG 222  
 |||  
 370 pGlu 371

seq\_name: SwissProt\_40:METK\_THEMA

## seq\_documentation\_block:

ID METK\_THEMA STANDARD; PRT; 395 AA.

AC O9X1Y8;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
 adenosyltransferase) (Adomet synthetase) (MAT).  
 GN METK OR TM1658.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogales; Thermotoga.  
 OX NCBI\_TaxID-2336;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-MSB8 / DSM 3109;  
 RX MEDLINE-99287316; PubMed-10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
 RA Haft D.H., Hickley E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett K.M.,  
 RA Stewart A.M., Cotton M.D., Pratt W.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RT genome sequence of Thermotoga maritima.";  
 RT Nature 399:323-329(1999)

CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 CC methionine and ATP. The overall synthetic reaction is composed of  
 CC two sequential steps, Adomet formation and the subsequent  
 CC triphosphatase hydrolysis which occurs prior to release of  
 CC Adomet from the enzyme (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC dihydrophosphate + S-adenosyl-L-methionine.

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```

CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE001807; AAD36725.1; -.
CC HSSP: P04384; IMXB.
CC TIGR: TML658; -.
CC InterPro: IPR002133; S-Adomet_synt.
CC Pfam: PF00438; S-Adomet_synt2; 1.
CC Pfam: PF02772; S-Adomet_syntD3; 1.
CC DR PFam: PF02772; S-Adomet_syntD3; 1.
CC DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
CC DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
CC KM Transferase: One-carbon metabolism; ATP-binding; Magnesium;
CC Complete proteome.
CC NP_BIND 270 277 ATP (POTENTIAL).
CC FT METAL 16 16 MAGNESIUM (BY SIMILARITY).
CC FT METAL 282 282 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 395 AA; 43673 MW; 5ACA50F1DA60A9D5 CRC64;

```

```

alignment_scores:
  Quality: 74.00      Length: 18
  Ratio: 4.625       Gaps: 0
Percent Similarity: 88.889 Percent Identity: 72.222

```

```

alignment_block:
US-09-198-779b-1 x METK_THEMA ..

```

```

Align seg 1/1 to: METK_THEMA from: 1 to: 395

```

```

169 AAGACCGCGCATGACGCGCATTTGGCGGACGACGCGCATTCACCTG 218
|||||
364 LysThrAlaIatYrGLyHisPheGLyArgAsnGluGluPheIrrTr 380
219 CGAG 222
|||
380 pGIu 381

```

```

seq_name: SwissProt_40:METK_ACACA

```

```

seq_documentation_block:
ID METK_ACACA STANDARD: PRT; 388 AA.
AC Q95032;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase).
OS Acanthamoeba castellanii (Ameoba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236447; PubMed=9116037;
RA Ahn K.S., Henney H.R. Jr.;
RT "Nucleotide sequence and developmental expression of Acanthamoeba
RT S-adenosylmethionine synthetase gene.";
RL Biochim. Biophys. Acta 1351:223-230(1997)
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +

```

```

CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X79205; CAA55794.1; -.
CC HSSP: P04384; IMXB.
CC InterPro: IPR002133; S-Adomet_synt.
CC Pfam: PF00438; S-Adomet_synt; 1.
CC DR Pfam: PF02772; S-Adomet_syntD2; 1.
CC DR Pfam: PF02773; S-Adomet_syntD3; 1.
CC DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
CC DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
CC KM Transferase: One-carbon metabolism; ATP-binding.
CC NP_BIND 120 125 ATP (POTENTIAL).
CC SQ SEQUENCE 388 AA; 42617 MW; 7CA72AF37B24A408 CRC64;

```

```

alignment_scores:
  Quality: 68.00      Length: 21
  Ratio: 4.250       Gaps: 0
Percent Similarity: 76.190 Percent Identity: 61.905

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```

alignment_block:
US-09-198-779b-1 x METK_ACACA ..

```

```

Align seg 1/1 to: METK_ACACA from: 1 to: 388

```

```

169 AAGACCGCGCATGACGCGCATTTGGCGGACGACGCGCATTCACCTG 218
|||||
364 LysThrAlaIatYrGLyHisPheGLyArgAsnGluGluPheIrrTr 380
219 CGAGTGTCTCAAG 231
|||||
380 pGIuAlaProLys 384

```

```

seq_name: SwissProt_40:METK_BACSU

```

```

seq_documentation_block:
ID METK_BACSU STANDARD: PRT; 400 AA.
AC P54419; Q34566;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR METE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168 / PY79;
RX MEDLINE=96345628; PubMed=8755891;
RA Yocum R., Perkins J.B., Howitt C.L., Pero J.;
RT "Cloning and characterization of the metE gene encoding S-
RT adenosylmethionine synthetase from Bacillus subtilis.";
RL J. Bacteriol. 178:4604-4610(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98048467; PubMed=9387221;
RA Lapius A., Galleron N., Sorokin A., Ehrlich S.D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
RT in the 200 kb trnB-dnaB region.";
RL Microbiology 143:3431-3441(1997).

```

```
CC -! FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC tripolysphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -! COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -! PATHWAY: Activated methyl cycle.
CC -! SUBUNIT: Homotrimer (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U52812; AAB17066.1; -
DR EMBL: AF008220; AAC00242.1; -
DR EMBL: Z99119; CAB15033.1; -
DR HSSP: P04384; IMXB.
DR Subtilist; Bg11840; metK.
DR Interpro: IPR002133; S-Adomet synt.
DR Pfam: PF00438; S-Adomet synt; 1.
DR Pfam: PF02772; S-Adomet syntd; 1.
DR Pfam: PF02773; S-Adomet syntd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Trnsferase; One-carbon metabolism; ATP-binding; Magnesium;
DR Complete proteome.
KW NP_BIND
FT METAL 274 281 ATP (POTENTIAL).
FT METAL 19 19 MAGNESIUM (BY SIMILARITY).
FT METAL 286 286 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 26 26 S -> Y (IN REF. 1).
FT CONFLICT 111 111 Q -> P (IN REF. 1).
FT CONFLICT 140 140 A -> V (IN REF. 1).
SQ SEQUENCE 400 AA; 44042 MW; EF3D97DCD375714A CRC64;

alignment_scores:
Quality: 65.00 Length: 18
Ratio: 4.333 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 66.667

alignment_block:
US-09-198-779B-1 x METK_BACSU ..
Align seg 1/1 to: METK_BACSU from: 1 to: 400

169 AAGACGGCGGATAGCGGACCTTTGGCGGTGACGCGCGGACTTACCTG 218
:::|||||
368 GINTTAAATATyGlyHisPheGlyArgHisAspValAspLeuProTyr 384
219 CGAG 222
|||
384 pglu 385

seq_name: SwissProt_40:METK_STRST
seq_documentation_block:
ID METK_STRST STANDARD; PRT; 411 AA.
AC 09X402;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK.
```

```
OS Streptomyces spectabilis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=68270;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27741;
RA Hyun C.G., Suh J.W.;
RT "Cloning of the gene for S-adenosyl-methionine synthetase from
RT Streptomyces spectabilis."
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
CC -! FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC tripolysphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -! COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -! PATHWAY: Activated methyl cycle.
CC -! SUBUNIT: Homotrimer (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: AF117274; AAD2464.1; -
DR HSSP: P04384; IMXB.
DR Interpro: IPR002133; S-Adomet synt.
DR Pfam: PF00438; S-Adomet synt; 1.
DR Pfam: PF02772; S-Adomet syntd; 1.
DR Pfam: PF02773; S-Adomet syntd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Trnsferase; One-carbon metabolism; ATP-binding; Magnesium.
KW NP_BIND
FT METAL 277 284 ATP (POTENTIAL).
FT METAL 17 17 MAGNESIUM (BY SIMILARITY).
FT METAL 289 289 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 411 AA; 44658 MW; FC87DD5811CDB355 CRC64;

alignment_scores:
Quality: 64.00 Length: 20
Ratio: 4.000 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 60.000

alignment_block:
US-09-198-779B-1 x METK_STRST ..
Align seg 1/1 to: METK_STRST from: 1 to: 411

163 TTCATCAAGACCGCGGATAGCGGACCTTTGGCGGTGACGCGGCGGACTT 212
:::|||||
369 TYRserGlnThrAlaIatyrGlyHisPheGlyArgSerLeuProGluPh 385
213 CACCTGCGAG 222
|||
385 ethrtpglu 388

seq_name: SwissProt_40:METK_HUMAN
seq_documentation_block:
ID METK_HUMAN STANDARD; PRT; 395 AA.
AC P31153;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
```

```

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine
GN MAT2A OR MAT2A2 OR AMS2.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93050159; PubMed=1426235;
RT "Horikawa S., Tsukada K.;
RT "Molecular cloning and developmental expression of a human kidney S-
RT adenosylmethionine synthetase.";
RL FEBS Lett. 312:37-41(1992).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT
CC FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA
CC AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY
CC DISTRIBUTED IN EXTRAHEPATIC TISSUES.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X68836; CAA48726.1; -.
DR PIR: S27257; S27257.
DR HSSP: P04384; IMXB.
DR MIM: 601468; -.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 131 136 ATP (POTENTIAL).
FT BINDING 159 159 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 43660 MW; 2E7D1B91C4AF7BDD CRC64;

alignment_scores:
Quality: 63.00 Length: 21
Ratio: 3.938 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 66.667

alignment_block:
US-09-198-779b-1 x METK_HUMAN ..
Align seg 1/1 to: METK_HUMAN from: 1 to: 395

169 AAGACCGCGCATACGGCACTTGGCGGTGACGACGCGCATTCACCTG 218
:::|||||
373 AAGTATTAATAATYTGlyHisPheGlyArgasp.....SerPheProtr 387
|||||
219 CGAGGTGCTCAAG 231
|||||
387 pgluValProlys 391

seq_name: SwissProt_40:METK_RAT
seq_documentation_block:

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ID METK_RAT STANDARD; PRT; 395 AA.
AC P18298;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine
GN MAT2A OR AMS2.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=90337979; PubMed=1696256;
RA Horikawa S., Sasuga J., Shimizu K., Ozasa H., Tsukada K.;
RT "Molecular cloning and nucleotide sequence of cDNA encoding the rat
RT kidney S-adenosylmethionine synthetase.";
RL J. Biol. Chem. 265:13683-13686(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA HIRAKI T., Horikawa S., Tsukada K.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT
CC FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA
CC AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY
CC DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM
CC PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY
CC REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J05571; AAA42106.1; -.
DR EMBL: AB000717; BAA19170.1; -.
DR EMBL: AB000716; BAA19170.1; JOINED.
DR PIR: A37118; A37118.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 131 136 ATP (POTENTIAL).
FT BINDING 159 159 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 43715 MW; 4DA9AFA8F7D09C79 CRC64;

alignment_scores:
Quality: 63.00 Length: 21
Ratio: 3.938 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 66.667

alignment_block:
US-09-198-779b-1 x METK_RAT ..
Align seg 1/1 to: METK_RAT from: 1 to: 395

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```

CC CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collabor
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstat
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CC CC modified and this statement is not removed. Usage by and for commec
CC CC entities requires a license agreement (See http://www.isb-sib.ch/anno
CC CC or send an email to license@isb-sib.ch).
CC -----
CC CC EMBL; AE000540; AAD07267.1; -.
CC CC HSSP; P04384; IMXB.
CC CC TIGR; HP0197; -.
CC CC InterPro; IPR002133; S-Adomet_synt.
CC CC Pfam; PF00438; S-Adomet_synt.1.
CC CC Pfam; PF02772; S-Adomet_syntD2; 1.
CC CC Pfam; PF02773; S-Adomet_syntD3; 1.
CC CC PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
CC CC PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
CC CC Transfaser; One-carbon metabolism; ATP-binding; Magnesium;
CC CC Complete proteome.
CC CC FT NP_BIND 260 267 ATP (POTENTIAL).
CC CC FT METAL 18 18 MAGNESIUM (BY SIMILARITY).
CC CC FT METAL 272 272 MAGNESIUM (BY SIMILARITY).
CC CC SEQUENCE 385 AA; 42362 MW; B1262A82075ADB5A CRC64;

alignment_scores:
    Quality: 61.00 Length: 17
    Ratio: 4.357 Gaps: 0
    Percent Similarity: 82.353 Percent Identity: 64.706

alignment_block:
US-09-198-779B-1 x METK_HELPY ..

Align seg 1/1 to: METK_HELPY from: 1 to: 385

172 ACCGCCGATACGGCCACTTGGCCGTCAGACGACGCCGACTTCACCTGGCA 221
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
355 ThrseraIatYrGLYhIsphedIyrgsIuengIugIuphethrTrpG1 371

222 G 222
|||
371 u 371

seq_name: SwissProt_40:METK_STRAU

seq_documentation_block:
ID METK_STRAU STANDARD; PRT; 397 AA.
AC P50307;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Tremblay A., Sasarman A.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC triphosphosphate hydrolysis which occurs prior to release of
CC CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC -1- diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).

```

```
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
```

DR EMBL, U36379; AAA79506.1; -.
DR HSSP, P04384; LMXB.
DR InterPro, IPR002133; S-Adomet\_synt.
DR Pfam, PF00438; S-Adomet\_synt.1.
DR Pfam, PF02772; S-Adomet\_synt2; 1.
DR Pfam, PF02773; S-Adomet\_synt3; 1.
DR PROSITE, PS00376; ADOMET\_SYNTHETASE\_1; 1.
DR PROSITE, PS00377; ADOMET\_SYNTHETASE\_2; 1.
DR Transferase; One-carbon metabolism; ATP-binding; Magnesium.
KW NP\_BIND 273 280 ATP (POTENTIAL)
FT METAL 19 19 MAGNESIUM (BY SIMILARITY).
FT METAL 285 285 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 397 AA; 43591 MW; 4D3E222FA04EB758 CRC64;

alignment\_scores:
Quality: 61.00 Length: 18
Ratio: 4.357 Gaps: 0
Percent Similarity: 77.778 Percent Identity: 66.667

alignment\_block:
US-09-198-779B-1 x METK\_STRAU ..
Align seg 1/1 to: METK\_STRAU from: 1 to: 397

169 AAGACCGCGCATACGGCCACTTTGGCCGAGCAGCGGACTTCACCTG 218
:::|||||
367 GlnThrAlaAlaIatYrGlnIsPheGlyArGThrAspValGluLeuProTr 383
219 CGAG 222
|||
383 pGlu 384

seq\_name: SwissProt\_40:METK\_BACHD
seq\_documentation\_block:
ID METK\_BACHD STANDARD; PRT; 399 AA.
AC 09K709;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR BH3300.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI\_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Mieno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
methionine and ATP. The overall synthetic reaction is composed of

```
CC two sequential steps, Adomet formation and the subsequent
CC triphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O -> phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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```

DR EMBL, AF001518; BAB07019.1; -.
DR HSSP, P04384; LFUG.
DR InterPro, IPR002133; S-Adomet\_synt.
DR Pfam, PF00438; S-Adomet\_synt.1.
DR Pfam, PF02772; S-Adomet\_synt2; 1.
DR Pfam, PF02773; S-Adomet\_synt3; 1.
DR PROSITE, PS00376; ADOMET\_SYNTHETASE\_1; 1.
DR PROSITE, PS00377; ADOMET\_SYNTHETASE\_2; 1.
DR Transferase; One-carbon metabolism; ATP-binding; Magnesium;
KW Complete proteome.
FT NP\_BIND 276 283 ATP (POTENTIAL).
FT METAL 21 21 MAGNESIUM (BY SIMILARITY).
FT METAL 288 288 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 399 AA; 43795 MW; 51C9A4DCEAD5329 CRC64;

alignment\_scores:
Quality: 61.00 Length: 18
Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment\_block:
US-09-198-779B-1 x METK\_BACHD ..
Align seg 1/1 to: METK\_BACHD from: 1 to: 399

169 AAGACCGCGCATACGGCCACTTTGGCCGAGCAGCGGACTTCACCTG 218
:::|||||
370 GlnThrAlaAlaIatYrGlnIsPheGlyArGThrAspValGluLeuProTr 386
219 CGAG 222
|||
386 pGlu 387

seq\_name: SwissProt\_40:METK\_LACIA
seq\_documentation\_block:
ID METK\_LACIA STANDARD; PRT; 399 AA.
AC 09CE00;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR L11902.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI\_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;

RA Bolotin A., Winkler P., Mauger S., Jallion O., Malarne K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*  
 RT *lactis* ssp. *lactis* IL1403.";  
 RL Genome Res. 11:731-753(2001).  
 CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 CC methionine and ATP. The overall synthetic reaction is composed of  
 CC two sequential steps, Adomet formation and the subsequent  
 CC triphosphosphate hydrolysis which occurs prior to release of  
 CC Adomet from the enzyme (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC diphosphate + S-adenosyl-L-methionine.  
 CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion  
 CC bind per subunit (By similarity).  
 CC -1- PATHWAY: Activated methyl cycle.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 CC  
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 CC  
 DR EMBL: AE006419; AK06000.1; -  
 DR InterPro: IPR002133; S-Adomet\_synth.  
 DR Pfam: PF00438; S-Adomet\_synth. 1.  
 DR Pfam: PF02772; S-Adomet\_synth2; 1.  
 DR Pfam: PF02773; S-Adomet\_synth3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 DR Transferrase: One-carbon metabolism; ATP-binding; Magnesium;  
 KW Complete proteome.  
 KM NE\_BIND 274 281 ATP (POTENTIAL).  
 FT METAL 18 18 MAGNESIUM (BY SIMILARITY).  
 FT METAL 286 286 MAGNESIUM (BY SIMILARITY).  
 SO SEQUENCE 399 AA; 43017 MW; 9A8127F3A550447E CRC64;

Alignment\_scores:  
 Quality: 61.00 Length: 18  
 Ratio: 4.067 Gaps: 0  
 Percent Similarity: 83.333 Percent Identity: 61.111

Alignment\_block:  
 US-09-198-779B-1 x METK\_LACLA ..  
 Align seg 1/1 to: METK\_LACLA from: 1 to: 399

169 AAGACCGCGATACGCGCCACTTGGCCGCGAGACGCGCACTTCACCTG 218  
 ::::::::::::::::::::::::::::::::::::  
 368 GlnThrAlaAlaIaTyGlyHisPheGlyArgThrAspValGIuLeuProTr 384

219 CGAG 222  
 ::  
 384 pGlu 385

seq\_name: SwissProt\_40:METK\_MYCTU

seq\_documentation\_block:  
 ID METK\_MYCTU STANDARD; PRT; 403 AA.  
 AC P77899;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
 DE adenosyltransferase) (Adomet synthetase) (MAT).  
 GN METK OR RV1392 OR MT1437 OR MTCY2184.09.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Horsley T., Jagels K., Jorgensen A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.D., Rogers J.,  
 RA Ruster S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gilm M.U., Holt D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 CC methionine and ATP. The overall synthetic reaction is composed of  
 CC two sequential steps, Adomet formation and the subsequent  
 CC triphosphosphate hydrolysis which occurs prior to release of  
 CC Adomet from the enzyme (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC diphosphate + S-adenosyl-L-methionine.  
 CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion  
 CC bind per subunit (By similarity).  
 CC -1- PATHWAY: Activated methyl cycle.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 CC  
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 CC  
 DR EMBL: Z80108; CAB02194.1; -  
 DR EMBL: AE007015; AK45702.1; ALT\_INT.  
 DR HSSP: P04384; IMXB.  
 DR TIGR: MT1437; -  
 DR TubercuList: RV1392; -  
 DR InterPro: IPR002133; S-Adomet\_synth.  
 DR Pfam: PF00438; S-Adomet\_synth. 1.  
 DR Pfam: PF02772; S-Adomet\_synth2; 1.  
 DR Pfam: PF02773; S-Adomet\_synth3; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 DR Transferrase: One-carbon metabolism; ATP-binding; Magnesium;  
 KW Complete proteome.  
 KM NE\_BIND 280 287 ATP (POTENTIAL).  
 FT METAL 19 19 MAGNESIUM (BY SIMILARITY).  
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).  
 SO SEQUENCE 403 AA; 43046 MW; 2E18BE05D8267972 CRC64;

Alignment\_scores:  
 Quality: 61.00 Length: 20  
 Ratio: 4.067 Gaps: 0  
 Percent Similarity: 75.000 Percent Identity: 55.000



alignment\_block:  
US-09-198-779B-1 x METK\_MYCTU ..

Align seg 1/1 to: METK\_MYCTU from: 1 to: 403

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163 TTTCATCAAGACCGCCGATACGGCCACTTTGGCGGTGACGACGCGACTT 212
    ::::::::::::::::::::::::::::::::::::::::::::
372 TTTATATATATATATATATATATATATATATATATATATATATATATAT 388
213 CACCTGGGAG 222
    |||
388 uprotprglu 391

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seq\_name: SwissProt\_40:METK\_SYNY3

seq\_documentation\_block:

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ID METK_SYNY3 STANDARD: PRT: 426 AA.
AC P72871;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR SLI0927.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905221;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugijura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996)
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC triphosphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90901; BAA16887.1; ALT_INT.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; ATP-binding; Magnesium;
KW Complete proteome.
FT NP_0287 294 ATP (POTENTIAL).

```

```

FT METAL 24 24 MAGNESIUM (BY SIMILARITY).
FT METAL 299 299 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 426 AA; 45865 MM; 0DFEBB5785F5FA CRC64;

```

alignment\_scores:

```

Quality: 60.50 Length: 22
Ratio: 3.559 Gaps: 1
Percent Similarity: 77.273 Percent Identity: 59.091

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alignment\_block:

US-09-198-779B-1 x METK\_SYNY3 ..

Align seg 1/1 to: METK\_SYNY3 from: 1 to: 426

```

160 AGGTTTCATCAAG...ACCGCGCATACGCCACTTTGGCGGTGACGACGC 206
    ||||| ::::::::::::::::::::::::::::::::::::::
384 ArghetherglnaspValAlaAlaTatrglyHisphelglnrgnaspLe 400
207 CGACTTCACCTGGCAG 222
    ||||| ::|
400 uaspleuprotprglu 405

```

seq\_name: SwissProt\_40:METK\_TREPA

seq\_documentation\_block:

```

ID METK_TREPA STANDARD: PRT: 396 AA.
AC O83772;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR TP0794.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwynn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khaklaj H., Richardson D., Howell J.K., Chidambaram M., Uteback T.,
RA McDonald L., Artlisch P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC triphosphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----

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DR EMBL: AEO01250; AAC65758.1; -
DR HSSP: P04384; IMXB.
DR TIGR: TP0794; -
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase: One-carbon metabolism; ATP-binding; Magnesium;
KM complete proteome.
FT NE_BIND 264 271 ATP (POTENTIAL).
FT METAL 276 276 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 396 AA; 42990 MW; E532DD39B0BBE711 CRC64;

alignment_scores:
  Quality: 59.00 Length: 33
  Ratio: 2.565 Gaps: 2
Percent Similarity: 69.697 Percent Identity: 39.394

alignment_block:
US-09-198-779B-1 x METK_TREPA ..
Align seg 1/1 to: METK_TREPA from: 1 to: 396

160 AGGTTGATCAGACGCGCATACGCGCATTTGGCGGTGACGAC..... 204
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
355 ArgYrArGserThAlaValrGlYhIsPhGlyArgGluGlnPhePr 371
205 .....GCCGACTTCACCTGCGGAGTG.....GTCAAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
371 oTrpEluArGThrAspCysValGAspLeuGlnArGAlaValArGPro 387

seq_name: SwissProt_40:METL_RAT

seq_documentation_block:
ID METL_RAT STANDARD; PRT; 397 AA.
AC P13444;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE S-adenosylmethionine synthetase alpha and beta forms (EC 2.5.1.6)
DE (Methionine adenosyltransferase) (Adomet synthetase) (MAT-I/III).
DE MAT-I OR AMSI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Liver;
RX MEDLINE=90032633; PubMed=2806235;
RA Horikawa S., Ishikawa M., Ozasa H., Tsukada K.;
RT "Isolation of a cDNA encoding the rat liver S-adenosylmethionine
  synthetase.";
RL Eur. J. Biochem. 184:497-501(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Mato J.M.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
  METHIONINE AND ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -!- PATHWAY: ACTIVATED METHYL CYCLE.
CC -!- SUBUNIT: HOMOTETRAMER FOR THE ALPHA FORM (MAT-I); HOMODIMER FOR
  THE BETA FORM (MAT-III).
CC -!- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT
  FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA
  AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY
  DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM

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CC CC PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY
CC CC REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.
CC CC -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL: X15734; CA33754.1; -
DR EMBL: X60822; -; NOT_ANNOTATED_CDS.
DR PIR: S06114; S06114.
DR PIR: S18256; S18256.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase: One-carbon metabolism; Multiligene family; ATP-binding.
KM NP_BIND 132 137 ATP (POTENTIAL).
FT BINDING 160 160 ATP (POTENTIAL).
SQ SEQUENCE 397 AA; 43698 MW; AB47A8CCBB207BA CRC64;

alignment_scores:
  Quality: 59.00 Length: 21
  Ratio: 3.688 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 61.905

alignment_block:
US-09-198-779B-1 x METL_RAT ..
Align seg 1/1 to: METL_RAT from: 1 to: 397

169 AAGACCGCGCGCATACGCGCATTTGGCGGTGACGCGCATTCACGCG 218
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
375 LysThnAlaCysTrGlyhIsPhGlyArg.....SerGluPheProTr 389
219 CGAGTGCGTCAAG 231
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
389 pEluValProLys 393

seq_name: SwissProt_40:METK_BUCAL

seq_documentation_block:
ID METK_BUCAL STANDARD; PRT; 378 AA.
AC P57486;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
  adenosyltransferase) (Adomet synthetase) (MAT).
DE METK OR BU408.
GN Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
  OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
  OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
  Buchnera sp. Aps.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
  methionine and ATP. The overall synthetic reaction is composed of
  two sequential steps, Adomet formation and the subsequent

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CC tripolyphosphate hydrolysis which occurs prior to release of
CC AdoMet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AP001119; BAB13109.1; -.
CC InterPro: IPR002133; S-AdoMet_synth.
CC Pfam; PF00438; S-AdoMet_synth2; 1.
CC Pfam; PF02772; S-AdoMet_synth2; 1.
CC Pfam; PF02773; S-AdoMet_synth2; 1.
CC PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
CC PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
CC Transferrase; One-carbon metabolism; ATP-binding; Magnesium;
KW Complete proteome.
FT NP_BIND 260 267 ATP (POTENTIAL).
FT METAL 17 17 MAGNESIUM (BY SIMILARITY).
FT METAL 272 272 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 378 AA; 41706 MW; C2C12B90561B71C8 CRC64;

alignment_scores:
Quality: 58.00 Length: 14
Ratio: 4.462 Gaps: 0
Percent Similarity: 92.857 Percent Identity: 64.286

alignment_block:
US-09-198-779B-1 x METK_BUCAT ..
Align seg 1/1 to: METK_BUCAT from: 1 to: 378

163 TTCATCAAGACCGCGCATACGGCCATTGGCCGTGACGAC 204
:::|||||:::|||||:::
352 TyrleuLysThrAlaValTyrGlyHisheGlyArgLysGlu 365

seq_name: SwissProt_40:POLN_SOUV3

seq_documentation_block:
ID POLN_SOUV3 STANDARD; PRT; 1788 AA.
AC 004544;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Non-structural polyprotein [Contains: RNA-directed RNA polymerase
DE (EC 2.7.7.48); Thiol protease (EC 3.4.22.-); Helicase (2C like
DE protein)].
OS Southampton virus (serotype 3).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norwalk-like viruses.
OX NCBL_TaxID=37129;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93142023; PubMed=8380940;
RA Lambden P.R., Caul E.O., Ashley C.R., Clarke I.N.;
RT "Sequence and genome organization of a human small round-structured
RT (Norwalk-like) virus."
RL Science 259:516-519(1993).
RN [2]
RN REVIEWS.
RX MEDLINE=96088083; PubMed=8560774;
```

```
RA Lambden P.R., Liu B., Clarke I.N.;
RT "A conserved sequence motif at the 5' terminus of the Southampton
RT virus genome is characteristic of the Caliciviridae."
RL Virus Genes 10:149-152(1995).
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C37.
CC -----
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CC -----
CC EMBL; L07418; AAA92983.1; -.
CC PIR; A37491; A37491.
CC MEROPS; C37.001; -.
CC InterPro: IPR004004; Calici_pol_hel.
CC InterPro: IPR000605; RNA_helicase.
CC InterPro: IPR001205; RNA_pol_p3d.
CC Pfam; PF00680; RNA_dep_RNA_pol; 1.
CC Pfam; PF00910; RNA_helicase; 1.
CC PRINTS; PR00918; CALICIVIRUS.
KW PRINTS; PR00917; SRVCYSPPTASE.
KW Polypeptide; Transferrase; RNA-directed RNA polymerase; Hydrolase;
KW Thiol protease; Helicase; ATP-binding.
FT CHAIN ? ? HELICASE (P2C-LIKE).
FT NP_BIND 714 1319 PROTEASE.
FT NP_BIND 561 568 ATP (BY SIMILARITY).
FT ACT_SITE 1238 1238 PROTEASE (BY SIMILARITY).
FT ACT_SITE 1236 1236 PROTEASE (BY SIMILARITY).
SQ SEQUENCE 1788 AA; 198581 MW; 9EDA6F6529793652F CRC64;

alignment_scores:
Quality: 57.50 Length: 55
Ratio: 2.130 Gaps: 2
Percent Similarity: 49.091 Percent Identity: 27.273

alignment_block:
US-09-198-779B-1/rev x POLN_SOUV3 ..
Align seg 1/1 to: POLN_SOUV3 from: 1 to: 1788

230 TTGACACACCTGCGAGTGAAGTCGGCGTCGTCACGCGCAAGTGGCCGTA 181
||||: ::|||:::|||||:::
253 LuserTyrAspGlnLeuLysGlnLeuGlnGluAsnGluPro...TriProty 268

180 TGGCGCGGTCTGTGATGACCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNN 131
|||||::: |||
268 rAlaAlaIleThrAsnAsnCys..... 275

130 NNNNNNNNAAGTACGCTGTTGTCGTCGTCATATATACACATTATA 81
::: ||||| :::
276 .....PheGluPheCysGlnValMetAsnLeuGlnAspThrTrp 289

80 ACACAACGAACAATG 66
|||||:::
290 LeuGlnArgArgLeu 294

seq_name: SwissProt_40:CLT2_HUMAN

seq_documentation_block:
ID CLT2_HUMAN STANDARD; PRT; 346 AA.
AC 09NS75; 09HC02;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cysteinyl leukotriene receptor 2 (CysLTR2) (P5ECO146) (HG57) (HPN321).
DE CysLTR2 OR CysLTR2 OR CysLTR2.
OS Homo sapiens (Human).
OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=20374466; PubMed=10913337;  
 RA Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,  
 RA Nishikawa T., Kawai Y., Masuho Y., Isegaki T., Suzuki Y., Sugano S.,  
 RA Furuchi K.;  
 RT "The molecular characterization and tissue distribution of the human  
 RT cysteinyl leukotriene CysLT2 receptor.";  
 RL Biochem. Biophys. Res. Commun. 274:316-322(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20459128; PubMed=10851239;  
 RA Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,  
 RA Im D.-S., Stocco R., Bellefleur J.N., Abramovitz M., Cheng R.,  
 RA Williams D.L., Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,  
 RA Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,  
 RA Lynch K.R., Evans J.F.;  
 RT "Characterization of the human cysteinyl leukotriene 2 receptor.";  
 RL J. Biol. Chem. 275:30531-30536(2000).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11093801;  
 RA Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,  
 RA Clivelli O.;  
 RT "Molecular cloning and characterization of a second human cysteinyl  
 RT leukotriene receptor: discovery of a subtype selective agonist.";  
 RL Mol. Pharmacol. 58:1601-1608(2000).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RA Dunn M.;  
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
 [5]  
 RP Suga H.;  
 RT "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";  
 RT Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is  
 CC mediated via a G-protein that activates a phosphatidylinositol-  
 CC calcium second messenger system. Stimulation by Bay u9773, a  
 CC partial agonist, induces specific contractions of pulmonary veins  
 CC and might also have an indirect role in the relaxation of the  
 CC pulmonary vascular endothelium. The rank order of affinities for  
 CC the leukotrienes is LTC4 > LTD4 > LTE4.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the  
 CC heart, placenta, spleen, peripheral blood leukocytes and adrenal  
 CC gland. In lung, expressed in the interstitial macrophages, and  
 CC slightly in smooth muscle cells.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 DR EMBL: AB038269; BAB03601.1; -  
 DR EMBL: AF254664; AAG17281.1; -  
 DR EMBL: AF279611; AAK69485.1; -  
 DR EMBL: AL137118; CAC29102.1; -  
 DR EMBL: AB041644; BAB16379.1; -  
 DR MIM: 605666; -  
 DR InterPro: IPR004071; CysLeuk\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR01533; CYSLTRCPTR.  
 DR PRINTS: PR00237; GPCR\_RHODOPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPT\_FL\_1; FALSE\_NEG.

DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_FL\_2. 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 43 63 1 (POTENTIAL).  
 FT DOMAIN 64 72 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 73 93 2 (POTENTIAL).  
 FT DOMAIN 94 123 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 124 144 3 (POTENTIAL).  
 FT DOMAIN 145 153 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 154 174 4 (POTENTIAL).  
 FT DOMAIN 175 204 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 205 225 5 (POTENTIAL).  
 FT DOMAIN 226 245 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 246 266 6 (POTENTIAL).  
 FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 287 307 7 (POTENTIAL).  
 FT DOMAIN 308 346 BY SIMILARITY.  
 FT DISULFID 111 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 346 AA; 39635 MW; EB54A4ADDE5EB4 CRC64;

alignment\_scores: Quality: 57.00 Length: 18  
 Ratio: 3.800 Gaps: 0  
 Percent Similarity: 83.333 Percent Identity: 50.000

alignment\_block:

US-09-198-779B-1/rev x CLT2\_HUMAN ..

Align seg 1/1 to: CLT2\_HUMAN from: 1 to: 346

64 ATCAGACCGTCATTATACAGATGCGAGCGTCGATCTGCCACGAG 15  
 :::::::::::::::::::::::::::::  
 266 LeuArgThrValHisLeuThrThrTrpLysValGlyLeuCysLysAspAr 282  
 14 GCTA 11  
 ||||  
 282 glen 283

